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AX068013 Sequence
AX068013 Nicotiana
U5661 Nicotiana
AX028012 Sequence
AX068019 Micotiana
AC13229 Liuteus tR
U40666 Nicotiana
AC134450 Micotiana
AC134450 Oryza sat
AR005514 Oryza sat
AZ0130728 Oryza sat
                                                               November 11, 2004, 06:56:19; Search time 3876.86 Seconds (without alignments) 10990.348 Million cell updates/sec
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	0.000	asterids;	lamids	 w	••	naceae; Nicotiana	da.
α <u>ί</u>	REFERENCE	Roitsch, T	.0.	•		4	`
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(II.)	FEATURES	g	Location/Qualif	3 2	alitlers	_	1
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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    DNA
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/organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
                                                                    Nicotiana tabacum (common tobacco)
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Goetz, M., Godt, D.E., Guivarc'h, A., Kahmann, U., Chriqui, D. and Roitsch, T.
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Direct Submission
Submitted (04-MAY-201) Plant Physiology and Cell Biology,
University of Regensburg, Universitaetsetr. 31, Regensburg 93053,
                                                                                                                                                                                                                    CCTATGATGGTAAGTACTTCTTCGTCCTTAATCAGAGGTTTCGACTTCGAGCTCCAGATA
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| /organism="Nin88" |
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Proc. Marl. Acad. Sci. U.S.A. (2001) In press
C bases 1 to 3293)
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98.1%; Score 883.8; DB 8;
Best Local Similarity 99.4%; Pred. No. 1.9e-151;
Matches 896; Conservative 0; Mismatches 4;
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db_xref="GI:14211754"
translation="M"
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7299 bp DNA linear PLN 12-JUN-2002 Nicotiana sylvestris Lhcbl*5, Lhcbl*6 genes for light harvesting AB012638
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Catresana, C., Staneloni, R.J., Malik, V.S. and Cashmore, A.R. Molecular characterization of two clusters of genes encoding Type I CAB polypeptides of PSII in Nicotiana plumbaginifolia Plant Mol. Biol. 10, 117-126 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 7299)

Hasegawa, K., Yukawa, Y., Sugita, M. and Sugiura, M.

Hasegawa, K., Yukawa, Y., Sugita, M. and Sugiura, M.

Submitted (27-MAR-1998) Masahiro Sugiura, Nagoya University, for Gene Research, Chikusa-ku, Nagoya, Aichi 464-8602, Japan (E-mail:h44979bauraccnagoya-u.ac.jp, Tel:+81-52-789-3081)
                                                                                    Cerdan, P.D., Staneloni, R.J., Casal, J.J. and Sanchez, R.A. A 146 bp fragment of the tobacco Lhcb1*2 promoter confers very low-fluence, low-fluence and high-irradiance responses phytochrome to a minimal CaMV 355 promoter Plant Mol. Biol. 33 (2), 245-255 (1997)
                                                                                                                                                                                                                       3 (bases 1 to 1705)
Stancloni, R.J. and Cerdan, P.D.
Direct Submission
Submitted (26-ARP-1996) R.J. Stancloni, Instituto de
Investigaciones Bioquimicas, Facultad de Ciencias Exactas y
Naturales (UBA), Av. Patricias Argentinas 435, Buenos Aires
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB012638.1 GI:3036947 a/b-binding protein. Light harvesting chlorophyll a/b-binding protein. Nicotiana sylvestris (wood tobacco) Nicotiana sylvestris (wood topacco) Subarayota viridiplantae, Streptophyta; Embryophyta; Tracheo Spermidophyta; eudicotyledons; core eudicots; sternids; lamiids; Solanales; Solanaceae; Nicotiana.
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Pred. No. 0.00029;
0; Mismatches 23;
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Matches 89; Conservative
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Nicotiana plumbaginifolia
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Epermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae, Nicotiana.
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1 (bases 1 to 3293)
Goetz, M., Godt, D.B., Guivarc'h, A., Kahmann, U., Chriqui, D. and Roitsch, T.
                                                                                                                                                                                                                                                                                                                                     Induction of male sterility in plants by metabolic engineering of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (04-MAY-2001) Plant Physiology and Cell Biology, University of Regensburg, Universitaetsstr. 31, Regensburg 93053,
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                      DNA linear PLN invertase Nin88 (Nin88)
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'product="extracellular invertase Nin88"

'protein.id="AAK57503.1"

'dD_xref="G1:14211754"

'translation="M"
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Proc. Natl. Acad. Sci. U.S.A. (2001) In press
C (bases 1 to 3293)
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60.3%; Pred. No. 0.0014;
iive 0; Mismatches 96;
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Nicotiana tabacum (common tobacco)
Nicotiana tabacum
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:4097"
1. 3290
/gene="Nin88"
<3291. .>3293
/gene="Nin88"
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Sequence 1 from Patent WO0077187.
                      AF376772S1 3293 bp
Nicotiana tabacum extracellular
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organism="Nicotiana
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                                                              promoter and partial cds. AF376772 GI:14211752
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/gene="Nin88"
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Matches 158; Conservative
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CRWAMLGALGCVFPELLARNGVKFGEAVWFXAGSQIFSEGGLDYLGNPSLVHAQSILA
IWACQVILMGAVEGYRVAGGPLGEVVDPLYPGGSFDPLGLAEDPEAFAELKVKEIKNG
                                                                                                                                                                                                                                                                                                                                       VSSGSPWYGPDRVKYLGPFSGESPSYLFGEFPGDYGWDTAGLSADPETFAKNRELEVI
HCRWAMLGALGCVFPELLARNGVKFGEAVWFKAGSQI FSEGGLDYLGNPSLVHAQSIL
AIWACQVVLMGAVEGYRVAGGPLGEVVDPLYPGGSFDPLGLAEDPEAFAELKVKEIKN
                                                                                                                                                                                                                                                                            'protein_id="BAA25392.1"
'db_xref="GI;3036948"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ranslation="MASSTMALSSSFAGKAVKLSPSSSEITGNGKVTMRKTASKAKPV
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/product="light harvesting chlorophyll a/b-binding
                                                                                                                                                                                                                                                                                                                                                                                 GRLAMFSMFGFFVQAITVTGKGPLENLADHLADPVNNNAWAYATNFVPGK"
complement(2572. .2673)
/gene="Lhcbl*6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1873. .2571)
/gene="Lhcb1*6"
/product="light harvesting chlorophyll a/b-binding
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.larity 79.5%; Pred. No. 0.00024;
Conservative 0; Mismatches 23; Indels 0
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/clone="lambda NSCBb1"
/tissue_type="leaf"
/tissue_type="leaf"
/clone_lib="lambda DASH genomic library"
/complement(1870, 22673)
                                                                                                                                                                                          'function="antenna complex"
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                                                                                                                                           complement (1870. .2673)
/gene="Lhcb1*6"
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complement(2760. .2767)
/note="Lhcb1*6
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/gene="Lhcb1*5"
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/note="putative"
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/gene="Lhcb1*5"
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/gene="Lhcb1*5"
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gene="Lhcb1*5"
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/note="Lhcb1*5
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
                            2819 icaaaaarcdaccaaaaaccdacraaagiiddicdciiiiiraaaaraiaiiiiraa
                                                                                       2759 ATTITITITITITITAGAAACCGACCAACAATTIGGICGGTITITITITITITITIGGCCAAAAATGC
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                                                                    ---TITIAITITIAATIGAAAACTAACCAAAGTIAGICGGIIITCTIGAAACATAAATITICG
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TAAATGATCCGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTTAATATTAATTTTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Nicotiana tabac
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
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Sequence 2 from Patent WO0077187.
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AX068013.1 GI:12329821
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AX068013/c
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AC090485/c
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VERSION
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                                                                      Nicotiana tabacum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                   366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 ---TITATITITAATIGAAAACTAACCAAAGTIAGTCGGTTTCTTGAAACATAAATTTCG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 CGGGACTCAAAATAGTTTTCCCGCATTTTTTGCGCCAAAGAAAACCGACCAAAGTTGGTCG 483
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                                                                                                                                                                          Promoter system and production and use of the same Patent: WO 007187-A 1 21-DEC-2000; Roitsch, Thomas, Dr. (DE) Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                           8.0%; Score 72.4; DB 6; ilarity 60.3%; Pred. No. 0.0014; Conservative 0; Mismatches 96;
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/organisa="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                                                                                                                                                                                                                                                                  /organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db xref="taxon:4097"
                                                 Nicotiana tabacum (common tobacco)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8 from Patent WO0077187.
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                  GI:12329820
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synthetic construct
artificial sequences.
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Best Local Similarity 60.3
Matches 158; Conservative
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Best Local Similarity
Matches 158; Conserv
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AX068012.1
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ACCESSION
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LAHGAALVPRHGGGGGCAASKRLPSYRLFAEHLLEPDQRAVAALASPRGSRLRPDVR
GLLAAYYAETANASFLCSHLLKDIEHIRLSYRPLKHTLRKLASDVGYSGLADVSAALG
GPTALAASQGRLREVQAGSGDLLRGLDAGRKKRHRIRSVARLRRALSVSFVTAVAV
VAVVGACIGVHILLAFAAFPMKSPANIGERFFSGRAARRLVQLEAAAKGTVILNRDN
ETISRLVARVRDEGEHMVALRRLCVEHRPAAGAGGKGRLVQEVLRQLSKNEESFRQQL
DELEEHLFLCFMTTNKARIMVMFWAAAAR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="mangnicklibelgavvlaersclokyofshgdvvlfkcpsdhre
LFVKRLIALPGEWMQLPGTPDIIKIPEGHCWVBGDNAACSWDSRSFGPEVDGIKDSMG
GVRVSSASGMIGPPRIPLGLIKGRVAHVIWPPSKIGRVDTKMPENRISPL"
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CKERCOTKKRKGSAMGEDVGDDSRSODRSHETTEVHYFNDKQDKAVEIKNILHDGVGQ
SPOGGOGLIDNBRRNGTVDKSR VDAHIDDKLGSGRDRNWTGKTQEPBGSVDYLRSCK
SQDSKEASDSEWKANGRROGGGFHRRVGYRRDFRGRSESTHGSSTYGSSYDFSDSIE
IRPNNSLDFGREGSVSGRYDVGVGAHRDVTYGTNGDKVTNSEPDQSGSASMISQFPQH
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LLPGVFVPPPPGGPLLWPGARGVDVNMLSVPPNLPIPPPVAGEHSFTPGMGAGPNIHL
NQFGSGIGAPTNMSGLSFHQLGTQSREMVHGKPPVGGGWTPNRNSGPTRKAPSRGEQN
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QHVLSPEFFGTKFDVILVDPPWEEYVHRAPGITDHIEYWNGEEIMNIKIEAIADTPSF
VFLMVGDGVGLEQGRQCLKKWGFRRCEDVCWVKTNKKSATPSLRHDSHTILQHSKEHC
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FGEDHNIRPGWLTLGKGLSYSNFNKEAYVKNPADKDGKVWQGGRNPPPEAPHLVVTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /noce="Similar to dbj|BAA88534.1| (AP000969) Similar to
Arabidopsis thaliana DNA chromosome 4, BAC clone T5L19
(AL049481) [Oryza sativa] Identities = 571/759 Evalue=
0.0; Similar to sp|P2553|KAR4 YEAST KARYOGAMY PROTEIN
KAR4 Identities = 98/328 Evalue= 2e-27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14781. .14815
// note="misc_rep03 similar to Rat tandem repeat mRNA"
complement(16551. .16787)
// note="Gaigin_O12 MITE element from gb:U72728 Oryza 1"
complement(17170. .17328)
// note="Wanderer_O85 MITE element from gb:X13679 Oryza"
                                                                                                                                                                                                                                                                                                     /note="Putative signal peptidase"

complement (join(3166. 3273,4313. .4387,5109. .5274,
5366. .3452,5534. .5556))
/note="%SJNBa0067N01.2"
/note="%Similar to emb|CAC09470.1| (AL442113) putative
singal peptidase [Oryza sativa] Identities = 68/138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Unknown protein with similarity to
methyltransferases and transcriptional regulators"
/protein.id="AKS8724.1"
/db_xref="G1:15451600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="Putative signal peptidase"
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db_xref="GI:15451599"
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|oin(19417. .20491,20573. .20916)
|gene="OSJNBa0067N01.4"
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'protein id="AAK98725.1"
'db xref="GI:15451601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="OSJNBa0067N01.3"
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                                                                                                                                                                                                                                                complement (3166. .5556)
/gene="OSJNBa0067N01.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3value= 7e-33"
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Palmer,L.E., de la Bastide,M., Spiegel,L., Preston,R., Kirchoff,K.,
King,L., Nascimento,L., Baker,J., Vil,M.D., Zutavern,T., Santos,L.,
Miller,B., Kuit,K., Cumlius,D.M., Rodriguez,S., Balija,V., Shah,R.,
McCombie,W.R.
                                                                                                                                                                                                                                                                                                                                   de la Bastide, M., Spiegel, L., Preston, R., Kirchoff, K., King, L., Nascimento, L., Baker, J., Vil, M.D., Zutavern, T., Santos, L., Baker, J., Vil, M.D., Zutavern, T., Santos, L., Shah, R., Baller, B., Kuit, K., Cunnius, D.M., Rodriguez, S., Balija, V., Shah, R., Bahret, A., Yang, C., Bell, M., Palmer, L., O'Shaughnessy, A., Dedhia, N. and McCombie, W.R. Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0067N01, from chromosome 3, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0067N01, from chromosome 3, complete sequence on Jun 20, 2001 this sequence version replaced gi:14209722.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data of (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                    Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 159636)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (06-SEP-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (24-FEB-2001) Lita Annenberg Hazen Genome Center, Cold Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor, NY 11724, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JUN-2001) Lita Annenberg Hazen Genome Center, Cold
Spring Harbor Laboratories, 1, Bungtown Road, Cold Spring Harbor,
NY 11724, USA
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F2J13.90 - Arabidopsis thaliana Identities = 119/339
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Mol type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
Genomic Sequence for Oryza sativa, Nipponbare strain, clone OSJNBa0067N01, from chromosome 3, complete sequence.
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/protein_id="AAK98722.1"
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/gene="OSJNBa0067N01.1"
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complement(851..931)
                                                                                            AC090485.3 GI:14495364
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hrzszzy7
Nicotiana tabacum lipid transfer protein gene, complete cds.
AF233297
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GGGNPSVPCCTGINNIYELAKTKEDRVAICNCLKNAFIHAGNVNPTLVAELPKKCGIS
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Pred. No. 0.0046;
0; Mismatches 304; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="lipid transfer protein"
/protein_id="AAF65316.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <654. .>1004
/product="lipid transfer protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism="Nicotiana tabacum"
                                                                                                                                                                         Nicotiana tabacum (common tobacco)
Nicotiana tabacum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xref="taxon:4097"
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/codon_start=1
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                                                                                                                                          QLEEQFKVKQIQLDKDVAGGMIEGGIREAQAGEGENEKTKKTQEGMÄDKSGTSQRVEN
ENEBEVIYTDEDEPRYQLVGSEENMESQESSDFAVAVGYVLSQTDEDMTEEKKKKSLRLM
EKEDKKVADAAAERKEALLMEINKDCALEAVDTNILNLIKNLELARINLFLKEKLNTSQ
KGECRNVGENLSNIDINIDEVLHSDDCMSDFDYAENMLRLSQSNLSGKKRKKNRGNL
EIFKVYPKCSGKNEKKKTKKKKS"
                                                                                                                                                                                                                                                                                                                                                                                                           /note="Putative retroelement"
join(21783. .22427,22632. .23195,23365. .23439)
join(21783. .22427,22632. .23195,23365. .23439)
foote="GSIMBAGO67N01.5"
/note="GSIMIJAT"
POL YPROTEIN [CONTAINS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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/protein id="A4X98766.1"
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/translation="WWWERKQEIMGKIEDIDKKCEAVGWTILERKERODLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEKIDEEKUYDNIKASITYKAMKAKAGFPDIMCHMILKVYKGGKVAIRVNYQIGHIFTT
HKGIRQGDPLSPLENIAADALTLIKKAAEQFDIMCHMILKVYKGGKVAIRVNYQIGHIFTT
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complement (25940. .26286)
/note="Tourist03 putative Tourist type MITE element"
complement (27827. .27898)
/note="Wanderer Osl MITE element from gb:L28995 Oryza"
complement (28675. .29018)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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/product=id=18489727.1"
/db_xref="G1:15451603"
/
                                                  EAVGRLHEVMYTVEGLPDEMKDYDPLHEVGSNLGPVI EVDMVSLKTKDVVRIRVGMYT
LKSLPLTMTLVTPKLLVYKAHLKLEQIVELGWFRDCAQEKRAVEVVEQNBPSNIDHMQ
RNKKPRKEEAASSMGVLEKAGDKKKAIVVEEDSDNESAQAELVKLKQMEIDRELALRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKKVVREDBLKWAGRCKEKNLLEGDDNTKYYHAKANGRKRKMNIYSLDGEDGEIKGOS
DLMKYITNPYKQLFGPPPENDFTLNLEGIAMLSEAEKERLIRPIEMEELKKVVFGMEN
NKAPGPDGFPVEFYKHFWYLIKDDLMELIIDFMKRKIGVERLNYGVITLIPKCKEAGI
                            translation="MQEKGVFHMRFPNKMKLDELAEFDSIRVKGTSVHVKVKKWTQEA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to gb|AAC24385.1| (U89959) Hypothetical protein [Arabidopsis thaliana] Identities = 333/556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="G340 Oryza sativa repetitive element G340 gi\mid5"
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/gene="OSJNBa0067N01.5"
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/note="Class_6712"
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RESULT 12 AF233297/c

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Genisteae,
                                                                                                                                                                                                                     Nuc.P., Nuc,K., Szweykowska-Kulinska,Z. and Pawelkiewicz,J.
Nucleotide sequence of nuclear tRNA(Gly) genes and tRNA(Gly)
seadogenes from yellow lupin (Luupinus luteus): expression of the
tRNA(Gly) genes in vitro and in vivo
Acta Biochim. Pol. 44 (2), 259-274 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (12-MAY-1995) Nuc P. W., University of Agriculture, Biochemistry & Biotechnology, ul.Wolynska 35, Poznan, Poland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol type="genomic DNA"
/cultivar="ventus, line no. 098067, Poland, Wiatrowo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On May 8, 1997 this sequence version replaced gi:1924956.
Location/Qualifiers
1. 7869
/organism="Lupinus luteus"
L.luteus tRNA-Gly genes and tRNA-Gly pseudogenes
                                  749255.1 GI:2073451
pseudogene; transfer RNA-Gly; tRNA-Gly gene.
Lupinus luteus (yellow lupine)
Lupinus luteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="epicoty1"
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323. .6668
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anticodon=(pos:364. .366,aa:Gly)
evidence=experimental
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6201. .6271
/gene="tRNA-Gly"
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|gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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gene="tRNA-Gly"
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                                                                                                                          1791 AATTTAGCGACCAACTTTGGTCGCTTTTCTTGATAAACCAACTTTGGTCGCTAAAGTTTG 1732
                                                                                                                                                                                                                                                                                                                 PLN 03-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission Shusei Sato, Kazusa DNA Research Institute, Submitted (12-NOV-2003) Shusei Sato, Kazusa BNA Research Institute, Department of Plant Gene Research; 2-6-7 Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan (E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/, Tel:81-438-52-3935(ex.2337),
                                         1849 AGTAGTGACCGATCTTGGTCGCTAATGTATA--TCAAATAATCATTTTTATTATTTCGCC 1792
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Sukaryota, Viridiplantae; Streptoophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
      592
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                                                                                       533 CAACTITAGICGGITITITIGGICGAITITITIGACCGACCAAAGIIGGICGGICGACCIIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="LjT31E21"
/clone lib="LjT library"
/note="TAC clone:TM0340, synonym:Lotus japonicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Lotus corniculatus var. japonicus"
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1. ,120480
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118; Conservative
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Nicotiana alata isolate S2S2 S-like RNase gene, intron sequence.
U40606
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                                                                                                                                                                                                                                                                                                                                                            156 ATTCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTATAC 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana alata (Persian tobacco)
Nicotiana alata
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 623)
Dodds, P.N., Clarke, A.E. and Newbigin, E.
Molecular characterisation of an S-like RNase of Nicotiana alata that is induced by phosphate starvation
Plant Mol. Biol. 31 (2), 227-238 (1996)
                                                                                                                                                                                                  36 TTAAATTCAAAAAAAAAAAAAAAAAAACCGACCAAAGTTGATCGGTATTTAATTA 95
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275. .481
275. .481
/note="instrion sequence found in the intron region
represents an allelic variant"
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Submitted (14-NOV-1995). Peter N Dodds, Botany, University of
Melbourne, Parkville, Victoria, 3052, Australia
1. .628
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                                                                                                                    7.6%; Score 68.8; DB 8; Length 7869; ilarity 59.0%; Pred. No. 0.0057; Conservative 0; Mismatches 82; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Nicotiana alata"
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1. ...628
/gene="S-like RNase gene"
6201. .6271
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/product="tRNA-Gly"
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600 TITGCCGAATTICTAGTAGTGACCGTGTAAGCTTCGGGAGAAATTITGTATATGT 659

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419 TATGTGTAGTATCAAGGGATTACCGGACACCGTAAACTTCGGCATAAACCTTGTATATGT 360
                                                                               660 ATATGTGTATATCCTTAAAATGATTAAATTTTAAAGAACGNNGCACCCTGAATACTAGAAGC 719
                                                                                                                 359 TTAACTACATACCTTAAAAATGATT-ATATAAATAACTTGGCACCCTAAACGTTAAAANC 301
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November 11, 2004, 06:24:54; Search time 444.342 Seconds (without alignments) 10644.348 Million cell updates/sec
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1 tggtcggaaattaccgacca......atgacttcatctgatttctc 901
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                             4134886 seqs, 2624710521 residues
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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genesedn2000s:* genesedn2001as:*

	Description	Aaf25735 Tobacco i	Aaf25742 Tobacco p				Aaf25736 Tobacco i	Adb87452 Transgene			Adj35283 Thale cre		Adl96879 STablizin	Ab132085 Human imm	Abl34172 Human imm	Abl34624 Human met		Aal54538 Arabidops	Adq24856 Human sof	Abl33776 Human imm	Abk28297 DNA trans	Abl34091 Human imm
	αī	AAF25735	AAF25742	AAF25736	AAF25735	AAF25742	AAF25736	ADB87452) ADB87474	ADJ35261	ADJ35283	ADL97593	ADL96879	ABL32085	ABL34172	ABL34624	ABL70607	AAL54538	2 ADQ24856	ABL33776	ABK28297	ABL34091
	DB	4	4	4	4	4	4	2	10	12	12	12	12	ø	φ	φ	v	10	12	9	9	9
	Query Match Length	3294	4135	4312	3294	4135	4312	1140	1140	1140	1140	1140	1140	5945	15518	15518	15518	91608	6816	6239	6239	5407
æ	Query Match	99.8	99.8	99.8	8.0	8.0	8.0	7.2	7.2	7.2	7.2	7.2	7.2	7.1	7.0	7.0	7.0	6.9	6.3	6.1	6.1	6.1
	Score	0000	899	899	72.4	72.4	72.4	64.8	64.8	64.8	64.8	64.8	64.8	64	62.8	82.8	62.8	61.8	57	55.4	55.4	55.2
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Abz10246 Haematopo	Aas60046 Human can		_		Abk31270 Signal tr	Abl70231 Chemicall	Aas61178 Human gen	Abx46069 Bovine ES	Abl55643 AmEPV gen	Ada71938 Rice gene	Aai83451 Human pol	Abl70316 Chemicall	Aas61254 Human gen	Abl32586 Human imm	Abk31228 Signal tr		Abk28234 DNA trans	Adi73089 Human ova		Abl33625 Human imm	Abv09124 Human pro	Abz10042 Haematopo	Ade84086 Human lym	
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ALIGNMENTS

Tobacco; tapetum-specific; pollen-specific; promoter; seed; invertase; male-sterile plant; in vitro embryogenesis; seedless fruit; transgenic plant; ds. Tobacco invertase promoter SEQ ID NO 1. AAF25735 standard; DNA; 3294 BP. (first entry) Nicotiana tabacum WO200077187-A2. 06-APR-2001 21-DEC-2000. RESULT AAF2573

13-JUN-2000; 2000WO-DE001944.

12-JUN-1999; 99DE-02009998. 04-APR-2000; 2000DE-02005992. 26-APR-2000; 2000DE-02007494. (ROIT/) ROITSCH T.

WPI; 2001-080685/09.

Roitsch T;

New tapetum- and pollen-specific promoter from tobacco, useful for preparing male sterile plants, particularly those with seedless fruits.

Claim 3; Page 64-65; 74pp; German.

This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a) expression system containing at least one (I); (b) nucleic acid construct (III) containing (I) part part of an expressible nucleic acid (III); (c) vector containing (I), the system of (a), or (II); (d) calls, particularly plant cells, containing (I), the system of (a), (II) or the vector of (c); (e) plants containing cells of (d); (f) seeds from the

plants of (e); (g) hybrid seed produced by crossing a male sterile plant of (e); (h) production of male sterile plants by introducing (II) into a cell and regeneration to a plant; (i) restorer plants contening in one (or preferably many) cells a construct (IIa) of (I) and a sequence that cencedes an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa); (k) seeds from plants of (e), (i) and (j); and (m) method for cloning a promoter that is functionally homologous with (II. Constructs containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a heterologous invertase-encoding sequence are used to prepare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) (I) can also be used to prepare transgenic plants that show increased or production of endogenous materials, e.g. of plant hormones or provide high level expression in a tissue- and time-specific manner, and contains or provide high level expression in a tissue- and time-specific manner, and contains or provide high level expression in a tissue- and time-specific manner, and contains the require expense transgenic plants to chemicals) for contains the require expense transgenic temperature or chemicals) for contains the require expense transgenic temperature or chemicals) for contains the require expense transgenic temperature or chemicals) for contains the require expense transgenic temperature or chemicals) for contains the contains t ${}^{8}_{6}$

Sequence 3294 BP; 983 A; 597 C; 644 G; 1064 T; 0 U; 6 Other;

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2434 2494 ö 2374 2554 2614 2734 2794 regressantracesaceaecriresresereariraarreaaaaaaaarreraa 2314 2674 2854 2855 TTGCCGAATTTCTAGTAGTGACCGAACCCTGTAAGCTTCGGGAGAAATTTTGTATATGTA 2914 240 300 480 600 AAAAAACCGACCAAAGTTGATCGGTATTTTAATTATGTAATAAAAAGATTCACTATCTGG 120 GAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACCACTAGACCATTGGTTCA 180 420 540 ATTITITAAATGATCCGCCGAATTAACCGACCAATTITGGTAGGTTTTTTAATAA 360 9 AAAAAACCGACCAAAGTTGATCGGTATTTTAATTATGTAATAAAAAGATTCACTATCTGG TITIGETITIAAGACTGTCTTTTATTTGATTTATACTCTTTAAATTATATTTTTGCGGAAA GAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACCACTAGACCATTGGTTCA TITIGITITAAGACTGTCTTTTATTTTGATTTATACTCTTTAATTATATTTTTGCACGAAA ATTITITIAAATGATCCGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTAATAATAATAA TITITATITATITAATIGAAAACTAACCAAAGTIAGICGGITICITGAAACAIAAATI TCGCGGGACTCAAAAAAAAAAAAGTTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGG 2675 TCGCGGGACTCAAAATAGTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGG rcggrircgraaaaaaaaaaaarrraaaaarararrrraaaaaaccgaccaacrira 601 TTGCCGAATTTCTAGTAGTGACCGAACCCTGTAAGCTTCGGGAGAAATTTTGTATATGTA TTTTTATTTATTTAATTGAAAACTAACCAAAGTTAGTCGGTTTCTTGAAACATAAATT TCGGTTTCGTAAAAAAAAAAAAATTTAAAAATATATTTTAAAAAACCGACCAACTTTA Gaps ; 0 99.8%; Score 899; DB 4; Length 3294; llarity 100.0%; Pred. No. 1e-171; Conservative 0; Mismatches 0; Indels (Similarity Query Match Best Local Simi Matches 901; 2255 61 121 2375 2435 241 2495 301 2555 361 2615 421 481 2735 181 g

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RES AAF ID	SULT 2 F25742 AAF25742	standard; DNA; 4135 BP.
X X	AAF257	
Y L	06-APR-2	001 (first entry)
X E X	Tobacco	promoter/invertase NIN88 DNA fragment SEQ ID NO 8.
		Tobacco; tapetum-specific; pollen-specific; promoter; seed; invertase; male-sterile plant; in vitro embryogenesis; seedless fruit; transgenic plant; ds.
SO.	Nicotiana	tabacum.
Y A. S	WO200077187	87-A2.
¥63		000
PF YX	13 - JUN-	2000- 2000WO-DE001944.
PR PR PR	12-JUN-1 04-APR-2 26-APR-2	999; 99DE-02009998. 000; 2000DE-02005992. 000; 2000DE-02007494.
X & S	(ROIT/)	ROITSCH T.
Y I	Roitsch T	
\$ # \$	WPI; 2001	-080685/09.
{	New tapetum preparing m	um- and pollen-specific promoter from tobacco, useful for male sterile plants, particularly those with seedless fruits.
PS XX	Example 4	.3; Page 68-70; 74pp, German.
888	This inve	This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a)
888	expressio (II) cont	n system containing at least one (I); (b) nucleic acid construct aining (I) plus at least part of an expressible nucleic acid
388	particula	<pre>// Vector containing (1), the system of (a), or (11); (d) cells, // Yplant cells, containing (1), the system of (a), (11) or the // // // A) alark containing (1), the system of (a), (f) order // // // // // // // // // // // // //</pre>
ខូខូខូ	plants of of (e); (e)	(v), (e) prairs Containing Cerrs O. (a); (l) seeus iron in the containing Cerrs O. (a); (g) hybrid seed produced by crossing a male sterile plant (l) production of male sterile plants by introducing (II) into a
881	cell and (or prefe	regeneration to a plant; (i) restorer plants containing in one rably many) cells a construct (IIa) of (I) and a sequence that
388	plant that (k) see	encodes an invertease alterent from the plants endogenous invertease; (3) plant that contains in one (or preferably wany) cells both (II) and (IIa); (K) seeds from plants of (i) and (j), (l) fruits, particularly
ប្រ	seedless,	produced by plants of (e), (i) and (j); and (m) method for

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cloning a promoter that is functionally homologous with (I). Constructs containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a heterologous invertase-encoding sequence are used to prepare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) diploid plants, and the new plants particularly produce seedless fruits. (I) can also be used to prepare transgenic plants that show increased or proteins involved in provision of energy to developing tissue. (I) provide high level expression in a tissue- and time-specific manner, and do not require exogenous stimuli (e.g. temperature or chemicals) for
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Seguence 4135 BP; 1212 A; 774 C; 825 G; 1318 T; 0 U; 6 Other;

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2854 2314 2434 ATTITITITAAATGATCCGCCGAATTAACCGACCAATTITITITITITITAATATTAA 2614 TIGCCGAATTICTAGTAGTGACCGAACCCTGTAAGCTTCGGGAGAATTITGTATATGTA 2914 TATGTGTATATCCTTAAAATGATTAAATTTAAAGAACGNNGCACCCTGAATACTAGAAGCC 2974 TITAGGGGCACTAGATGAGCAGAATAACGTGTTCTCGTCGCGTAAAAATACTTGGATCCG 3034 2374 redecidio de la respecta de la comparta del comparta de la comparta del comparta de la comparta del comparta de la comparta del comparta de la comparta del comparta del comparta de la comparta de la comparta de la comparta del comparta de la comparta de la comparta de la comparta del comparta de la comparta de la comparta del comparta TCGGTTTCGTAAAAAAAAAATTTAAAAATATATTTTAAAAAACCGACCAACTTTA 2794 riricirriaagacigicirriairingarriaracicirraarrarririrgcacgaaa 2494 720 780 600 120 300 540 TIGCCGAATITICIAGIAGIGACCGAACCCIGIAAGCIICGGGAGAATITIGIAIAIGIA 660 180 240 ATTITITIAAATGATCCGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTAATATTAA 360 TTTTTATTTTATTTAATTGAAAACTAACCAAAGTTAGTCGGGTTTCTTGAAACATAAATT 420 TCGCGGGACTCAAAATAGTTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGG 480 9 Gregerritiegregaritireaceaaceaagrigeregeregeregeregeregere TATGTGTATATCCTTAAAATGATTAAATTTAAAGAACGNNGCACCCTGAATACTAGAAGCC TITAGGGGCACTAGATGAGCAGAATAACGTGTTCTCGTCGCGTAAAAATACTTGGATCCG 2255 recressaarracceaccaacrrigerecearraarraaarreaaaaaaararreaaa AAAAAACCGACCAAAGTTGATCGGTATTTTAATTATGTAATAAAAAGATTCACTATCTGG GAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACCACTAGACCATTGGTTCA TITIGITITIAAGACIGICITITIAITITGAITITATACICITITAATIAITITITIGCACGAAA Gaps .; 0 Length 4135; 0; Indels Score 899; DB 4; Le Pred. No. 1.1e-171; 99.8%; Scor. 100.0%; Pred. No. 1.-Matches 901; Conservative Query Match Best Local Similarity 2315 121 2375 2435 241 2495 2555 2615 421 2675 2735 601 2855 2915 61 661 721 Н 181 301 361 481 541 2795

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New tapetum- and pollen-specific promoter from tobacco, useful for preparing male sterile plants, particularly those with seedless fruits.

Claim 6; Page 65-66; 74pp; German.

This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a) expression system containing at least part of an expressible nucleic acid construct (II) containing (I) plus at least part of an expressible nucleic acid construct (II) containing (I) plus at least part of an expressible nucleic acid construct (II); (c) vector containing (I), the system of (a), (II) or the particularly plant containing (I), the system of (a), (II) or the vector of (c); (a) plants containing cells of (d), (f) seeds from the plants of (e); (g) hybrid seed produced by crossing a male sterile plant of (f), (h) production of male sterile plants of (e); (h) production of male sterile plants of (e); (h) production of male sterile plants containing in one cell and regeneration to a plant; (i) restorer plants containing in one (or preferably many) cells a construct (IIa) of (I) and a sequence that condess an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa) (k) seeds from plants of (i) and (j); and (m) method for cloning a promoter that is functionally homologous with (I). Constructs containing (I) and an invertase-encoding sequence are used to produce heterologous invertase-encoding sequence are used to produce there while constructs that contain (I) and a better while constructs that contain (I) and containing (I) allow propagation of the male-sterile plants are used for in vitro embryogenesis of haploid or (double) these plants, and the new plants particularly produce seedless fruits.

3154 3035 ccrargargaradracrictrecretrareacaggrireactregagerecagara 3094 840 Tobacco; tapetum-specific; pollen-specific; promoter; seed; invertase; male-sterile plant; in vitro embryogenesis; seedless fruit; 3095 TAAACTATAGACTCGTCTTTATAGCACCTTTTTAATAAGACTATGACTTCATCTGATTTCT CCTATGATGGTAAGTACTTCTTCGTCCTTAATCAGAGGTTTCGACTTCGAGCTCCAGATA TAAACTATAGACTCGTCTTTATAGCACCTTTTAATAAGACTATGACTTCATCTGATTTCT Tobacco invertase promoter SEQ ID NO 2. 12-JUN-1999; 99DE-02009998. 04-APR-2000; 2000DE-02005992. 26-APR-2000; 2000DE-02007494. 13-JUN-2000; 2000WO-DE001944. AAF25736 standard; DNA; 4312 (first entry) transgenic plant; ds WPI; 2001-080685/09. Nicotiana tabacum. (ROIT/) ROITSCH 3155 C 3155 WO200077187-A2. C 901 06-APR-2001 21-DEC-2000. Roitsch T; AAF25736; 841 781 901 RESULT 3 **AA**F2573 g ò ò

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(I) can also be used to prepare transgenic plants that show increased or reduced production of endogenous materials, e.g. of plant hormones or proteins involved in provision of energy to developing tissue. (I) provide high level expression in a tissue- and time-specific manner, and do not require exogenous stimuli (e.g. temperature or chemicals) for
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Tobacco invertase promoter SEQ ID NO 1.
                                                                                                                                                                                                       Claim 3; Page 64-65; 74pp; German.
                           AAF25735 standard; DNA; 3294
                                                                                                                         13-JUN-2000; 2000WO-DE001944.
                                                                                                                                        04-APR-2000; 2000DE-02005992.
26-APR-2000; 2000DE-02007494.
                                                (first entry)
                                                                           male-sterile plant; i
transgenic plant; ds.
                                                                                                                                                                             WPI; 2001-080685/09.
                                                                                                                                                         (ROIT/) ROITSCH T.
                                                                                         Nicotiana tabacum
 4173
                                                                                                    WO200077187-A2.
                                                                                                                                    12-JUN-1999;
                                                06-APR-2001
                                                                                                               21-DEC-2000
 4173 C
                                      AAF25735;
                                                                     Tobacco;
                      AAF25735/
                 RESULT
                           d
                                                                                                                                                                                                                                                                                                                                                                         4172
                                                                                                                                                                                                                                                                                                                                                                     1113 TAAACTATAGACTCGTCTTTATAGCACCTTTTTAATAAGACTATGACTTCCATCTGATTTCT
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This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a) expressible mothering at least part of an expressible nucleic acid construct (II) containing (I) plus at least part of an expressible nucleic acid (III); (c) vector containing (I), the system of (a), or (II); (d) cells, particularly plant cells, containing (I), the system of (a), (iI) or the vector of (c); (e) plants containing (I), the system of (a), (iI) or the vector of (c); (e) plants containing cells of (d); (f) seeds from the plants of (e); (g) hybrid seed produced by crossing a male sterile plant of (e); (h) production of male sterile plants by introducing (II) into a cell and regeneration to a plant; (i) restorer plants containing in one (or preferably many) cells a construct (IIa) of (I) and sequence that contains in one (or preferably many) cells both (II) and (IIa) of plant that contains in one (or preferably many) cells both (II) and (IIa) of (k) seeds from plants of (i) and (j); (l) fruits, particularly containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a invertase-encoding sequence are used to prepare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) diploid plants, and the new plants particularly produce seedless fruits.

(I) can also be used to prepare transgenic plants that show increased or reduced production of endogenous materials, e.g. of plant bowning or provide high level expression in a tissue and time specific manner, and the new plants energy to developing tissue. (I) remile involved in provision of endogenous and time specific manner, and the new lants energy to developing tissue.
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preparing male sterile plants, particularly those with seedless fruits.
                                                                                                                                                                                                                                                                                                                                                                  tapetum-specific; pollen-specific; promoter; seed; invertase;
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Sequence 3294 BP; 983 A; 597 C; 644 G; 1064 T; 0 U; 6 Other;

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transgenic plant; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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04-APR-2000;
26-APR-2000;
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                                                                                                                                                TCAAAAAATCGACCAAAAAACCGACTAAAGTTGGTCGGTTTTTTAAAATTTTTTTAA 2760
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                                                                                                                                                                                                                                   2759 ATTTTTTTTTTTTAAGGAAACCGACCAACTTTGGTCGGTTTTCTTTGGCGCAAAATGC
                                                                                                                                                                                                                                                                                                                      GGGAAACTATTTTGAGTCCCGCGAAATTTATGTTTCAAGAAACCGACTAACTTTGGTTA
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                                                                                                                                                                                                                                                                              CGGGACTCAAAATAGTTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGGTCG
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                                                                                                         TAAATGATCCGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTAATATTAATTTTTA-
                                                               Gaps
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60
                    Length 3294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tobacco promoter/invertase NIN88 DNA fragment SEQ ID NO 8.
                                                               Indels
                    Score 72.4; DB 4; 1
Pred. No. 3.2e-05;
0; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTTAATTCGGCGGATCATTTA 2562
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2000DE-02005992.
2000DE-02007494.
                    8.0%;
al Similarity 60.3%;
158; Conservative
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26-APR-2000;
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                        Query Match
Best Local S
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Matches
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IID AAF22/C
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cor preferably many) cells a construct (IIa) of (I) and a sequence that encodes an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa); (k) seeds from plants of (e) (i) and (j); and (m) method for cloning a promoer that is functionally bomologous with (I). Constructs containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a loop functionally encoded to prepare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) (I) can also be used for in vitro embryogenesis of haploid or (double) reduced production of endogenous materials, e.g. of plant hormones or reduced production of endogenous materials, e.g. of plant hormones or provide high level expression in a tissue- and time-specific manner, and contain (e.g. temperature or chemicals) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2819 icaaaaarcgaccaaaaaaccgacraaagricgicggriririraaaarararririaa 2760
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:le plant; in vitro embryogenesis; seedless fruit;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 72.4; DB 4; Length 4135; 60.3%; Pred. No. 3.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96; Indels
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2000DE-02005992.
2000DE-02007494.
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Transgene expression regulatory element, STAR A13
                04-DEC-2003
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                                                                                                                                                                                                 This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a) expressible system containing at least one (I); (b) nucleic acid construct (II) containing (I) plus at least part of an expressible nucleic acid particularly plant cells, containing (I), the system of (a), or (II); (d) cells, particularly plant cells, containing (I), the system of (a), (II) or the vector of (c); (e) plants containing (I), the system of (a), (II) or the vector of (b); (g) hybrid seed produced by crossing a male sterile plant of (a); (b) production of male sterile plants by introducing (II) into a cell and regeneration to a plant; (i) restorer plants containing in one (or preferably many) cells a construct (IIa) of (I) and sequence that encodes an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa); (k) seeds from plants of (i) and (j); (l) fruits, particularly seedless, produced by plants of (e), (i) and (j); and (m) method for containing a prometer that is functionally homologous with (I). Constructs containing prometer that is functionally homologous with (I). Constructs containing prometer that is functionally produce seed to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a hard an invertase-encoding sequence are used to prepare response these plants are used for in vitro embryogenesis of haploid or (double) diploid plants, and the new plants particularly produce seedless fruits.

(I) can also be used to prepare transgenic plants that show increased or reduced production of endogenous materials, e.g. of plant horsenes or proteins involved in provision of energy to developing tissue. (I) contrained by the require expension or energies themselves and the new plants the subsection of themselves or provide high level expression in a tissue- and time-specific manner, and the new pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3777 ATTÍTÍTÍTÍTÍTÍTÍTÁTAGGÁÁÁCGACCÁÁCTÍTÍGGÍCGGÍTÍTÍTCÍTTGGCGCÁÁÁAATGC 3718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3717 GGGAACTATTTTGAGTCCCGCGAAATTTATGTTTCAAGAAACCGACTAACTTTGGTTA 3658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAAAAAATGGACCAAAAAACGGACTAAAGTTGGTCGGTTTTTTAAAATATATTTTTTAA 3778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGGGACTCAAAATAGTTTCCCGCATTTTTGCGCCAAAGAAACCGACCAAAGTTGGTCG 483
                                                                                                             New tapetum- and pollen-specific promoter from tobacco, useful for
preparing male sterile plants, particularly those with seedless fruits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---TITATITITAATIGAAAACTAACCAAAGTIAGICGGTITCTIGAAACATAAATITCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAATGATCCGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTTAATATTAATTTTTA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.0%; Score 72.4; DB 4; Length 4312; 60.3%; Pred. No. 3.3e-05; tive 0; Mismatches 96; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4312 BP; 1196 A; 827 C; 905 G; 1382 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGTTAATTCGGCGGATCATTTA 3580
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                                                                                                                                                                      Claim 6; Page 65-66; 74pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                         WPI; 2001-080685/09
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ses 158; Conserv
(ROIT/) ROITSCH T.
                                    Roitsch T,
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Matches
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The invention relates to DNA sequences with gene transcription regulatory qualities and methods for the detection and use of the regulatory DNA sequences. The invention further comprises providing a transcription system with a variety fragment-comprising vectors; and performing a selection step in the transcription system in order to identify a fragment comprising the DNA sequence with the gene transcription modulating activity. This polynucleotide represents a STAR element used in the method of the invention. The STAR element is shown to improve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 ITTAATTATTTTTGCACGAAAATAACCGACCAAAGTTGGTCGATTTTATTAAAAAGTA
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gene transcription; regulatory; variety fragment; STAR element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene transcription; regulatory; variety fragment; STAR element;
transgene expression; ds,
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ilarity 60.0%; Pred. No. 0.00096;
Conservative 0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 43; Fig 26; 216pp; English.
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05-JUL-2001; 2001US-0303199P.
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                                    transgene expression; ds
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Les 108; Conserv
                                                                                                                                               WO2003004704-A2
                                                                                           Unidentified
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217

187

ADB87452 standard; DNA; 1140 BP

ADB87452/c

ADB87452;

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14-JUN-2002; 2002EP-00077344.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         rcaragercaargeaccageccagaarcaacccagarcracararcaraccaragararara 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTATACTC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAR affiliated proteinaceous molecule; post translational modification; thale cress; stabilising anti-repression; STAR; STAR element; ds.
                                                                                                                                                                               Selecting a DNA sequence with a gene transcription modulating quality by providing a transcription system with a variety fragment-comprising vectors and performing a selection step in the transcription system.
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0
                                                                                                                                                                                                                                                                                                                                                                          Score 64.8; DB 10; Length 1140;
Pred. No. 0.00096;
0; Mismatches 72; Indels 0;
                                                                                                                                                                                                                                                                                                                                                    Sequence 1140 BP; 357 A; 221 C; 186 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stabilising anti-repression, STAR, element #13.
                                                                                                                                                                                                                            Claim 43; Fig 26; 216pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2002; 2002WO-NL000390
                                                                                     04-JUL-2001; 2001EP-00202581
05-JUL-2001; 2001US-0303199P
                                                                                                                                                                                                                                                                                                                                                                           7.2%;
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 60.0
Matches 108; Conservative
                                                                                                                                          Otte AP, Kruckeberg AL;
                                                                                                                     (CHRO-) CHROMAGENICS BV.
                                                                                                                                                                                                                                                                                                                                    transgene expression.
                                                                                                                                                             WPI; 2003-229412/22.
                        WO2003004704-A2
   Unidentified
                                             16-JAN-2003
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The invention relates to a method of producing a proteinaceous molecule (I) in a cell comprising selecting a cell for its suitability for producing (I), providing a nucleic acid encoding (I) with a nucleic acid comprising a STabilising Anti-Repression (STAR) sequence, expressing the resulting nucleic acid in the cell and collecting (I). The method is useful for producing (I). A cell line (II) provided with a nucleic acid comprising a STAR sequence Is useful for producing (I). (II) Enables production of affiliated proteinaceous molecule, as cell carries out proper post-translational modifications of produced proteins. The present sequence represents a thale cress stabilising anti-repression, STAR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157
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                                                                                                                                                                                                 Producing proteinaceous molecules in cells by selecting a cell, providing a nucleic acid encoding a proteinaceous molecule with an STabilizing Anti-Repression sequence and expressing proteinaceous molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTTGATTTATACTC 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 TAATAAAAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCAAGATACTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1140 BP; 357 A; 221 C; 186 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thale cress stabilising anti-repression, STAR, element #35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 64.8; DB 12; Length
Pred. No. 0.00096;
0; Mismatches 72; Indels
                                                                                                                                                                                                                                                                                                                                                   Example 13; SEQ ID NO 97; 177pp; English
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                                                                      Satijn DPE;
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Les 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL,
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(CHRO-) CHROMAGENICS
                                                                      Otte AP, Kruckeberg
                                                                                                                                      WPI; 2004-082195/08
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The invention relates to a method of producing a proteinaceous molecule producing cell comprising selecting a cell for its suitability for producing (I), providing a nucleic acid encoding (I) with a nucleic acid comprising a STabilishing Anti-Repression (STAR) sequence, expressing the resulting nucleic acid in the cell and collecting (I). The method is useful for producing (I). A cell line (II) provided with a nucleic acid comprising a STAR sequence Is useful for producing (I). (II) Enables production of affiliated proteinaceous molecule, as cell arrials proper post-translational modifications of produced proteins. The present sequence represents a thale cress stabilising anti-repression, STAR,
                Producing proteinaceous molecules in cells by selecting a cell, providing a nucleic acid encoding a proteinaceous molecule with an STabilizing Anti-Repression sequence and expressing proteinaceous molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 TAATAAAAAGATTCACTATCTGGGAATCGAACCGGGGGTCTGTACTATGGCAAGATACTAT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 TCTACCACTAGACCATTGGTTCATTTTGATTTAAGACTGTCTTTTATTTGATTTATACTC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rcaracrcaarccaccagccagaarcgaacccaggrcrcraccaracaagaaacrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTATAAAGTATCATGTAAAAACAACACAATCTTTTGTAGTTTGTACCAACTACGAAGTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Obtaining (MI) a cell which expresses two or more proteins, by providing cell with protein expression units encoding proteins, comprising protein expression units with STablizing Anti-Repressor sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein expression unit; STablizing Anti-Repressor; STAR; heterologous; multimeric; transgene expression; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 TCTACCACTAGACCACTGGTGCTTTTTTGATTAAACACGACTAAATATAATATAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 ITTAATTATTTTTGCACGAAAATAACCGACCAAAGTTGGTCGATTTTATTAAAAAGTA
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1140 BP; 357 A; 221 C; 186 G; 376 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 64.8; DB 12;
Pred. No. 0.00096;
0; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STablizing Anti-Repressor DNA sequence, A35
                                                                                              Example 13; SEQ ID NO 119; 177pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                        7.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0°
Matches 108; Conservative
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Example 14; SEQ ID NO 119; 213pp; English

Length 1140;

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           expresses two or more proteins. The method comprises providing the cell with two or more proteins. The method comprises providing the cell proteins, having at least two of the protein expression units with at least one Stablizing Anti-Repressor (STAR) sequence. The method provides lincassed predictability in the production of recombinant cell lines that effectively produce heterologous multimeric proteins of interest, increase the yield of heterologous multimeric proteins, stable expression of heterologous multimeric proteins, stable expression. This polynucleotide sequence represents the DNA of a STablizing Anti-Repressor (STAR) sequence of the invention.
                                                                                                                                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for obtaining a cell which expresses two or more proteins. The method comprises providing the cell with two or more protein expression units encoding the two or more protein expression units encoding the two or more proteins, having at least two of the protein expression units with at least one STablizing Anti-Repressor (STAR) sequence. The method provides increased predictability in the production of recombinant cell lines that effectively produce heterologous multimeric proteins of interest,
                                                                                                                                                                                                                                                                                                                                                                         307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein expression unit; STablizing Anti-Repressor; STAR; heterologous; multimeric; transgene expression; ds.
                                                                                                                                                                                                                                                                                                                                                                                                              TCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTTATACTC
                                                                                                                                                                                                                                                                                                                                   TAATAAAAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCAAGATACTAT
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invention relates to a novel method for obtaining a cell which
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                                                                                                                                                                                                                                                            Length 1140;
                                                                                                                                                                                                                       Sequence 1140 BP; 357 A; 221 C; 186 G; 376 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                          DB 12;
                                                                                                                                                                                                                                                          Score 64.8; DB 12
Pred. No. 0.00096;
                                                                                                                                                                                                                                                                              Pred. No. 0.00
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                                                                                                                                                                                                                                                            7.2%;
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nes 108; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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diseases. The present sequence is a gene of the invention

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increase the yield of heterologous multimeric proteins, stable expression of heterologous multimeric proteins and favorable transgene expression. This polynucleotide sequence represents the DNA of a STablizing Anti-Repressor (STAR) sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTACCACTAGACCATTGGTTCATTTTGTATTAAGACTGTCTTTTATTTGATTTATACTC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITAATITATATTITIGCACGAAATAACCGACCAAAGTIGGTCGATTITATTAAAAAGTA 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 ATTATAAAGTATCATGTAAAAACAACAACATCTTTTGTAGTTTGTACCAACTACGAAGTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiarturitic; antidabetic; antipsoriatic; antiarflammatic; antiartic; antilnflammatory; cancer; eye disease; articiosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                        rcaraccrcaarecaccaccaccaccaarcaacccccccrcrcraraccaraccara
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                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                       12; Length 1140;
                                                                                                                                                            Sequence 1140 BP; 357 A; 221 C; 186 G; 376 T; 0 U; 0 Other;
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                                                                                                                                                                                                                       Score 64.8; DB 12;
Pred. No. 0.00096;
0; Mismatches 72;
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                                                                                                                                                                                                                          7.2%;
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ABL32085 standard; DNA; 5945
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01-SEP-2000; 2000DE-01043826
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                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 108; Conserv
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                                                                                                     Repressor
                                                                                                                                                                                                                                                                                                                                                98
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ABL32085/c
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The present invention provides a number of human immune system associated dense which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and tractment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and mecular degeneration, arteriosclerosis, annemia, cancer, acute myeloid leukaemia, Albieimer's disease, AlbS. epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune system disease; cytosine methylation; antiasthmatic; antiatrefisoclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvisant; ophthalmologici; antirheumatic; antiarthritic; antidabetic; antipsoriatic; antiframmatory; cancer; eye disease; arteriosclerosis; anaemia; antiinflammatory; cancer; eye disease; atteriosclerosis; anaemia; acute myeloid leukaemia; Albrimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatold arthritis; psoriasis; bowel disease; gene;
                                                                                                                                92 ATTATGTAATAAAAGATTCACTATCTGGGAATCGAACCGGGGGTCTGTACTATGGCAAGA
                                                                                                                                                                                  5480 CAAAAATAAAAAACTCTTCTTTAACTAAAAACTAATTAAAAATACATAAAAATA
                                                                                                                                                                                                                                                                                        AAAGTAAAATTACTTACCAAAGTTGGTCGATTTTTTTAAATGATCCGCCGAATTAACCGA
                                                                                                                                                                                                                                                                                                                                                                      332 CCAATTTTGGTAGGTTTTTTTAATATTATTTTTTATTTTTAATTTGAAAACTAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 TCAATTAAATTCAAAAAAAAATATTGTAAAAAAAAAAACCGACCAAAGTTGATCGGTATTTTA
                                                                                                                                                                                                                                      5300 AAATCTCAAAAACAATAAAATAAAAAAAAAATTTTCTCACAAGCCCACACGTATAACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGTTAGTCGGTTTCTTGAAACATAAATTTCGCGGGACTCAAAAATAGTTTCCCGCATTT
                                                                                                                                                                                                          152 TACTATICTACCACTAGACCATTGGTTTTTTTTTTAAGACTGTCTTTTATTTGATTT
                                                                            Gaps
                         Sequence 5945 BP; 2043 A; 23 C; 1010 G; 2869 T; 0 U; 0 Other;
                                                  Length 5945;
                                                                           0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 2145.
                                                   Score 64; DB 6.
Pred. No. 0.001
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                                                     7.18;
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                                                                           223; Conservative
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                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 AATATATT
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                                                                                                                                 The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid rebunancia Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                           fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
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                                                                                                                                                                                                                                            Query Match, 7.0%; Score 62.8; DB 6; Length 15518; Best Local Similarity 46.6%; Pred. No. 0.0032; Matches 234; Conservative 0; Mismatches 267; Indels 1;
                                                                                                                  claim 1; SEQ ID NO 2145; 32pp + Sequence Listing; German
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from chemically treated metastasis genes, by analysis of cytosine methylation, also
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                                         cytostatic; gene therapy; ds.
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ID NO: 177
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Pred. No. 0.0032;
metastasis associated gene SEQ
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07-APR-2000; 200DEE-01019173.
30-JUN-2000; 2000DE-0103529.
01-SBP-2000; 2000DE-01043828.
                                                                                                                                                                                                                                                                                    06-APR-2001; 2001WO-EP003970
                                                 gene;
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(first entry)

26-MAR-2002

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Search completed: November 11, 2004, 08:10:27 Job time : 448.342 secs

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Run

IDENTITY_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Perfect score:

Seguence:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

995 - est 1.3 - est 1.3 - est 1.3 - est 2.3 - est 2.3 - est 2.3 - est 2.4 -

EST:*

Database

Length 1101; Score 75.4; DB 9; Pred. No. 5e-05; 8.4%; 39.9%; Query Match Best Local Similarity

ORIGIN

Drosophil ZUAH175TV

CNS020K7 AZ670108 CL539617 CL799614 CL829972 CNS00EVL CG962071 CNS00KHX

909 605 759 1101 642 905 748 818

DB

Length

Query

Score

Result No.

BZ413877 CC714001 BZ755113 BZ991051 CC335052 BQ648574 CC730035

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OSIIEa12E Tetraodon

AL099642 I CC993538 2 CB624068 C AL174271 1 CG054601 E

CC993538 CC993538 CB624068 CNS012GM CG054601 CG054598

757 7037 9037 919 836 845 1029 651

0 0 0 0 0

/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR05N11"
/clone lib="RRCI 98"
/note="end : TET3"

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01-SEP-2000
clone
                                                                                                                                                                   /mol_type="genomic DNA"

/db xref="taxon:3712"
/clone_lib="Boleracea@02"
/note="Vector: poTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea Tol000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
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Tetraodon nigroviridis genome survey sequence T7 end of clone
222L11 of library G from Tetraodon nigroviridis, genomic survey
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25.(2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 357 AAAACAGTITGACTIGCAAAATCACAAAGAAAACAIGCACCAGCCGGIAAICGAACCCG
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Characterization and repeat analysis of the compact genome of greatwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
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                                                                                                                                                   organism="Brassica oleracea"
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                                                                     High quality sequence stop: 521.
Location/Qualifiers
Plate: lla55 row: e column:
Seg primer: -21UPpOT forward
Class: shotgun
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AL175696.1 GI:7813753
GSS; genome survey sequence.
Tetracdon nigroviridis
Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing Center."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BZ088961 863 bp DNA linear GSS 10-OCT-2002 lla55e08.bl B.oleracea002 Brassica oleracea genomic, genomic survey
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                                                                                                                                                                                                                                                    154 CTATTCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTAT
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                                                34 AATTAAATTCAAAAAATATTGTAAAAAAAAACCGACCAAAGTTGATCGGTATTTAAT
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Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
Contact: Richard K. Wilson
  ÿ
  Mismatches 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
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                  - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Exa: 301 838 3543
Email: bjloftus@tigr.org
Clone; are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                               180 ATTTTGTTTTAAGACTGTCTTTTATTTGATTTATACTCTTTAATTATTATTTTTGCAGGAA 239
                                                                                                                                                                                                                                                                                                                                                                                                                   360 ATTITIATITATITAATTGAAAACTAACCAAAGTTAGTCGGTTTCTTGAAACATAAAT 419
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             660 TTTTWTAAAAAWWTTTTTTTTTTTWWWTTTAAAWATAAAWTTWAAAWDTTWAAAWDTTK 601
                                                                                                                                                     /organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="122111"
/note="Genoscope sequence ID : C0AG222CF06LP1~end : T7"
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Entamoeba histolytica
Entamoeba histolytica
Entamoebiae, Entamoeba.

1 (bases 1 to 909)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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0
                                                                                                                                                                                                                                                                                                              7.5%; Score 67.2; DB 9; Length 1092; 37.2%; Pred. No. 0.0022; Live 57; Mismatches 132; Indels 0
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Class: shotgun
High quality sequence start: 16
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605 bp DNA linear GSS 14-JUN-2004 OB Ba0051K04.f OB Ba Oryza brachyantha genomic clone CL539617
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Oryza brachyantha
Coryza brachyantha
Bukaryoza, Virigiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Virigiplantae, Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 605)
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 AATTA--TGTAATAAAAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCA
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Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Fal: 520 626 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77; Indels
                                                       'organism="Entamoeba histolytica"
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                                                                            'mol_type="genomic DNA"
'strain="HM1:IMSS"
High quality sequence stop: 784.
Location/Qualifiers
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les 125; Conservative
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Score 65.8; DB 9; Length 759;
Pred. No. 0.0042;
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/organism="Oryza rufipogon"
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| Organism="Oryza rufipogon"
| Organism="Oryza rufipogon"
| Organism="Oryza rufipogon"
| Organism="Oryza rufipogon"
| Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="Organism="
                                                                                                                                                                                                                                                   /mol_type="genomic DNN"
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30; Indels
Plate: 0051 row: K column: 04
Seg primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
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BACKWARD: CAC TCA TTA GGC ACC CCA
Blate: 010 row: O column: 01
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
                                                                                                                  Location/Qualifiers
1. .605
/organism="Oryza brachyantha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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Best Local Similarity 73.7%
Matches 84; Conservative
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CL799614
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/mol_trype="genomic DNA"
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/clone_lib="OR_CBa"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII;
drk treated 36 hrs before harvest"
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I (bases I to 760)

Kim, H., Yu, Y., Wissotski, M., Yost, D., Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Ming, R.
                                                           104 AAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACC 163
                                                                                                                                                                                 164 ACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTATACTCTTTAAT 223
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                                                                                                                   526 AAAAATGCACCAGCCGGAATCGAACCCGGGTCTGTACCGTGGCAGGGTACTATTCTACC
Gaps
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7.3%; Score 65.8; DB 9; Length 760;
Best Local Similarity 66.7%; Pred. No. 0.0042;
Matches 94; Conservative 0; Mismatches 47; Indels
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Unpublished (2004)
Contact: Rod A. Wing
Arizona demomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 625 955
Fax: 520 621 1259
Email: http://genome.arizona.edu
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BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0051 row: N column: 11
Seq primer: TAA TAC GAC TCA TAG GG
Class: BAC ends.
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CG962071 642 bp DNA linear GSS 15-DEC-2003 MBEDE79TRC mth2 Medicago truncatula genomic clone 31M13, genomic
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Medicago truncatula
Medicago truncatula
Medicago truncatula
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                           778 KAIWKWTANAAWTATATWWATATWWTWATTWTTWTTTTTATWTAAWTTATWT 719.
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                257 GGTCGATITITATTAAAAGTAAAATTACTTACCAAAGTTGGTCGATTTTTTAAATGATC 316
                                                                                                                                                                                                                                                                                                                                                                                                                             317 CGCCGAATTAACCGACCAATTTTGGTAGGTTTTTTAATATTATAATATTTTTAATATTTTAA
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Cook, D.R. and Kim, D.J, unpublished"
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Pred. No. 0.0047;
0; Mismatches 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Town,C.D., Shetty,J., Koo,H. and Feldblyum,T.F. Sequencing of BAC ends from Medicago truncatula Unpublished (2003)
Unbublished MEDE79TFC
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/cultivar="genotype A17"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
Seg primer: CAGGAAACAGCTATGACC
Class: BAC ends.
Location/Qualifiers
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Best Local Similarity 76.9%;
Matches 80; Conservative
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CG962071
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Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
BP 191006 EVRY cedex - FRANCE (5-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named REC1-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                    GSS 04-JUN-1999
end of BAC:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 TCGGTATTTTAATTATGTAATAAAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        958 AWANTITAATAANAATATWAWWWITTATITITITITITITITITATAWANAATATAIW 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 CTATGGCAAGATACTATTCTACCACTAGACCATTGGT----TCATTTTGTTTTAAGACTG 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTTTTATTTGATTTATACTCTTTAATTATATTTTGCACGAAAATAACCGACCAAAGTT 256
                        1101 bp DNA linear GSS 04-JUN-1: BACR29B23 of RPCI-98 library from Drosophila melanogaster genome survey sequence T7 end of BAC: fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTTGATTTATACTCTTTAAT
                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophildae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Drosophila melanogaster"
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/db xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="BACR29B23"
/clone lib="RPCI-98"
/note="end : T7"
                                                                                           TATATTTTGCACGAAATAA 244
                                                                                                                                    Trecergeaagegeaaacaa 666
                                                                                                                                                                                                                                                                                                                                                                   AL069706.1 GI:4949849
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Best Local S:
Matches 188
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                                                                                           224
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CNS00EVL/c
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Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (Dases 1 to 748)

E Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N., Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L., Caravern,T., McCombie,W.R. and Martienssen,R.A. Genomic shotgun sequences from Zea mays (methyl-filtered)

Lordavern,T., McCombie from Zea mays (methyl-filtered)

Lordavern,T., McCombie Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

Fax: 516 367 8884

Email: mcCombie@cshl.org

Plate: if18 row: e column: 02

Seg primer: -21M13UnivRev

Class: shotgun
                                                                                                                                                                                                                                                                                                                                                        if18e02.91 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone B2413877 GE355893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230
                                                                       110
                                 111 CACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACCACTAGAC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 CACCAGCCGGGAATCGAACCCGGGTCTGTACCGTGGCAGGGTACTATTCTACCACTAGAC 331
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/clone lib="WGS-ZmaysF (DH5a methyl filtered)"
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                                                                                                                                                                            508 AAAAAATATTTTAAAAACCGACCAA 535
                                                                                                                                                                                                                     538 MWMCWAACATTTATMAAMAMCAAWTAA 511
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/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 748.
Location/Qualifiers
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/clone="if18e02"
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/organism="Zea mays"
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Conservative
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                                     448
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosor in Pieter de Jons's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buiffalo, NY. The library is named RPCI-98 and was constructed by partial Ecost digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
                                                                                                                                                                                                                                        CNSOOKHX 905 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR17N06 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroida, Drosophilidae, Drosophila.

[ (bases 1 to 905)
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                                     595 CTACCACTAGACCACTGGTTTTGATGTTAAGGAGGTTTTAT
   CTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTT
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="BACR17N06"
                                                                                                                                                                                                                                                                                                                              fly), genomic survey sequence.
AL077798
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/note="end : T7"
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PUBNH65TD ZM 0.6_1.0 KB Zea mays genomic clone ZMMBTa094K10, genomic survey sequence.
BZ991051
BZ991051.1 GI:29232461
GSS.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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/clone="xxmxBra284B06"
/clone="taxmxm.o.6_1.0 KB"
/note="vector: pcR4-ToPO; Site_1: BcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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Mitclaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
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TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels
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Pred. No. 0.0056;
0; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Zea mays"
                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                               Tel: 301-838-5843
Fax: 301-838-0208
Emall: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                    Maize Genomics Consortium
Unpublished (2003)
Contact: Cathy Whitelaw
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Unpublished (2003)
                    GI:28907462
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Best Local Similarity 67.9%;
Matches 91; Conservative
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                                                                                                                                                                          CC714001 818 bp DNA linear GSS 19-JUN-2003
OGWDL09TV ZM 0.71.5 KB Zea mays genomic clone ZWHBMa0547A18,
genomic survey sequence.
CC714001
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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Whitelaw,C.A., Ouackenbush,J., Van Aken,S., Utterback,T.,
Whitelaw,C.A., Praser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citesk,R.W., Numberg,A., Robbins,D. and Lakey,N.
Unpublished (2002)
Other GsSs: OGWDLOFTH
Contact: Cathy Whitelaw
  CACTGGTGCATTTGTGCCTAAGTTCTTAAATGGGTTTGATTATAGGACCGTGCTACATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTATACTCTTTAATTATATTT
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Tel: 301-838-5843
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/strain="B73"
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/organism="Zea mays"
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Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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1 (bases 1 to 715)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Whitelaw, C.A., Praserr, C.M., Budiman, M.A., Bedell, J.A., Roblins, D. Consortium for Maize Genomics
Consortium for Maize Genomics
Contact: Cathy Whitelaw
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/dlone="ZMMBTa094K10"
/clone="Ib="ZM_06_1.0 KB"
/note="Yector: pGR4_TOF0; Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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/clone="b=zm_0"7_1.5_KB"
/note="vector: pBcSk-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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7.2%; Score 65.2; DB 8; Length 757;
Best Local Similarity 67.9%; Pred. No. 0.0056;
Matches 91; Conservative 0; Mismatches 43; Indels (
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Tel: 301-838-5843
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/mol_type="genomic DNA"
/strain="B73"
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/strain="B73"
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seg primer: TF
Class: sheared ends.
Location/Qualifiers
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Class: sheared ends.
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Fax: 301-838-0208
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Score 64.8; DB 8; Length 715;
Pred. No. 0.0068;
0; Mismatches 47; Indels (
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        7.2%;
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Best Local Similarity 66.4%
Matches 93; Conservative
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Sequence 32, Appl
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Sequence 12, Appl
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Sequence 131, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 30, Appl
Sequence 31, Appl
                                                          November 11, 2004, 07:45:44; Search time 92.8475 Seconds (without alignments) 6897.553 Million cell updates/sec
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1 tggtcggàaattaccgacca......atgacttcatctgatttctc 901
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. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
. /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
. /cgn2_6/ptodata/1/ina/Patrus_COMB.seq:*
. /cgn2_6/ptodata/1/ina/Patrus_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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US-09-328-475C-81
US-08-673-814-1
                                                                                                   US-10-009-966C-1_COPY_2255_3155
                                                                                                                                                                            824507 segs, 355394441 residues
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                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        nucleic search, using sw model
                                                                                                                                             IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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209 AAACAAAAATGCAAGAACCGGGAATCGAACCCGGGGCCCAACGATGGCAACGTTGGATT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Li, Xin-Liang
APPLICANT: Li, Xin-Liang
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Ljungdahl, Lars G.
APPLICANT: Chen, Huizhong
APPLICANT: Ximenes, Eduardo A.
TITLE OF INVENTION: Beta-glucosidase Coding Sequences and Protein from
TITLE OF INVENTION: Organicangles PC-2
FILE REFERENCE: 31-98us
CURRENT PPLICATION NUMBER: US/09/306,593
CURRENT FILING DATE: 1199-05-06
EARLIER APPLICATION NUMBER: US 60/084,494
BARLIER PILING DATE: 1988-05-06
SOFFWARE: PATENTIN OF: 2.0
SOFFWARE: PATENTIN OF: 2.0
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                                                                      159 CTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCT
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Pred. No. 0.11;
0; Mismatches 127;
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US-07-991-867B-32
Sequence 32, Application US/07991867B
Settent No. 5476781
GENERAL INFORMATION:
APPLICANT: MOYEr, Richard W.
APPLICANT: Hall, Richard L.
                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-306-593-1/c
; Sequence 1, Application US/09306593
; Patent No. 6184018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Orpinomyces sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (39)..(2009)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: mat_peptide
LOCATION: (87)..(2009)
                                                                                                                                                                                                                219 TT 220
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Best Local Simil
Matches 146; (
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US-09-306-593-1
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APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
RIOR FILING DATE: 1998-02-13
RIOR FILING DATE: 1998-03-13
RUMBER OF SEQ ID NOS: 28208
SEQ ID NO 7073
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 48.6; DB 4; Length 640681; Pred. No. 0.17;
                                                                                            APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SARKAI, YOSHIVUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-03-23
PRIOR APPLICATION NUMBER: JP2000-107160
NEAR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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llarity 62.3%; Pred. No. 0.026;
Conservative 0; Mismatches 46; Indels
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Best Local Similarity 48.4
Matches 135; Conservative
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Best Local Simi
Matches 76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 1
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69 GACCAAAGTTGATCGGTATTTTAATTATGTAATAAAAGATTCACTATCTGGGAATCGAA 128
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                                                                                                                               429 CTCAAAAATAGTTTCCCGCATTTTTGCGCCCAAAGAAAACCGACCAAAGTTGGTCGGTTTC 488
                                                                                                                                                                                           431 TICCTATIAGIATAGITIAAATATGGAATCAATACAAATAAAGAFTATAAATITA 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Michael B.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 45.8; DB 1; Length 6
Pred. No. 0.14;
0; Mismatches 282; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                               517
                                                                                                                                                                                                                                                                                                                               491 TAGAAAATTAATTAATTIAAAAAATTA 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-74N-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATOMAKE: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/CONCRET NUMBER: 31,794
REPRENCE (904) 372-5800
INPORMATION FOR SEQ ID NO: 32: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                               489 GTAAAAAAAAAAAATTTAAAAAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08107755A Patent No. 5721352
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 44.4
Matches 226; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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CLASSIFICATION:
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STATE: FI
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 CCAAAGTIGGTCGATTTTATTAAAAAGTAAAATTACTTACCAAAGTIGGTCGATTTTTTT 308
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APPLICANT: Gruidl, Michael E.
TITLE OF INVEXTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
CLASSIFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 10-JAN 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SALIMANCHIA, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: J1,794
REFERENCE/DOCKET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 282;
                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TYPE: nucleic acid
STRANDEDNESS: double
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Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                           ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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TELECOMMUNICATION INFORMATION:
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Best Local Similarity 44.4 Matches 226; Conservative
                                                                                                 nucleic acid
EDNESS: double
                                                                                                                                    unknown
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US-09-370-861A-32
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                                                    TAAGACTGTCTTTTATTTGATTTATACTCTTTAATTATTATTTTGCACGAAAATAACCGA
                                                                                                                     CCAAAGTTGGTCGATTTTAATAAAAGTAAAATTACTTACCAAAGTTGGTCGATTTTTTT
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Sequence 32, Application US/08544332
Patent No. 593577
GENERAL INFORMATION:
APPLICANT: MOYEN, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruid!, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSES: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patentin Release #1.0, Version #1.25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MBER: US 07/827,685
30-JAN-1992
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APPLICATION NUMBER: US/08/544,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US 07/657,584
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FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,66
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy
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Fatent No. 641021
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Moyer, Richard L.
TILE CPINT: Graid!, Michael E.
TILE REFERENCE: UF114.C4.D1
CURRENT APPLICATION NO. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UF114.C4.D1
CURRENT FILING DATE: 1990-08-09
PRIOR APPLICATION NUMBER: US/09/370,861A
PRIOR APPLICATION NUMBER: US 07/991,867
PRIOR APPLICATION NUMBER: US 02/107,755
PRIOR PAPLICATION NUMBER: WO 92/14818
PRIOR FILING DATE: 1993-08-19
PRIOR FILING DATE: 1993-08-19
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1993-08-19
PRIOR FILING DATE: 1992-01-30
PRIOR FILING DATE: 1992-01-30
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                                                                                                                                                                                                                                                                                                                                      Length 660;
                                                                                                                                                                                                                                                                                                                                      Score 45.8; DB 2; Length 6 Pred. No. 0.14; 0; Mismatches 282; Indels
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                                                                                                                                                                                                                       ) TOPOLOGY: unknown
) MOLECULE TYPE: DNA (genomic)
US-08-544-332-32
TELEPHONE: 904-375-8100
TELEFAX. 904-375-5600
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 660 base pairs
TYPE: nucleic acid
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1042 ТАТАТАТТТСАААТТТАААТАТТААТТТААТТТТҮАТТТАТААСААААТТТААААТАТАА 1101
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Pred. No. 0.17;
0; Mismatches 282; Indels
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                                                                           PRIOR APPLICATION 1939
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-0AN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
                                                                                                                                                                                                                                                          FILING DATE: 19-FEB-1991
ATTORNEX/ABENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REPRERNENCAPOOKET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 44.4%;
Matches 226; Conservative (
                                    12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1511 base pairs
  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                               904-372-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: doub
                      APPLICATION NUMB
FILING DATE: 11
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
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LOCATION:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-07-991-867B-8
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APPLICANT: Hall; Richard L.
APPLICANT: Hall; Richard L.
APPLICANT: Hall; Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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                                                                                                                                                                                                                Score 45.8; DB 4; Length 660;
Pred. No. 0.14;
0; Mismatches 282; Indels
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                                                                                                                                                  ; ORGANISM: Amsacta moorei entomopoxvirus
US-09-370-861A-32
PRIOR APPLICATION NUMBER: US 07/657,584 PRIOR FILING DATE: 1991-02-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DC
SOFTWARE: Patentin Release #11
                    PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                Query Match
Best Local Similarity 44.4%;
Matches 226; Conservative
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STATE: FL
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                                                                                  SEQ ID NO 32
LENGTH: 660
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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COUNTRY:
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Sequence 8, Application US/08107755A
Patent No. 5721352
GENERAL INFORMATION:
APPLICANT: Mayer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Similarity 44.4%; Pred. No. 0.17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                            ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CIIY: Gainesville
                                                                              1342 TAGAAAATTAATTAATTIAAAAAATTA 1370
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                                                NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFENCE/DOCKET NUMBER: UF114.C2
TELEPHONE: (904) 375-8100
TELEPHONE: (904) 372-5800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: LS11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRICE APPLICATION DATA:
APPLICATION WHERE: US 07/827,658
FILING DATE: 30-JAN-1992
PRICE APPLICATION UNDER: US 07/657,584
APPLICATION UNDER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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MEDLIW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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852..1511
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CLASSIFICATION:
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LOCATION:
FEATURE:
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Best Local Simi
Matches 226;
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US-08-107-755A-8
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69 GACCAAAGTTGATCGGTATTTTAATTATGTAATAAAAAGATTCACTATCTGGGAATCGAA
                                                                                                                          983 GCATATAATATTATGATAATA-ATATTTTAAATAATATTCCAGAAAATATTAAAAGTT
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Patent No. 5935777
GENERAL INFORMATION:
APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
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STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1342 TAGAAAATTAATTAATTTAAAAAATTA 1370
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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Sequence 8, Application US/09370861A Patent No. 6410221
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LENGTH: 19
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44.4%; Pred. No. 0.17;
tive 0; Mismatches 282;
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REGISTRATION NUMBER: 37,746
REDEPHONE: 904-375-8100
TELEPHONE: 904-375-800
TELEPHONE: 904-375-800
TELEPHONE: 904-375-800
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGHH: 1511 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
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Matches 226; Conservative
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852..1511
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LOCATION:
FEATURE:
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FEATURE:
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US-08-544-332-8
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RESULT 12 US-09-370-861A-8

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983 GCATATAATATTATGATAATA-ATATTTAAATAATATTCCAGAAAATATTAAAGTT 1041
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APPLICANT: Moyer, Richard W.
APPLICANT: Gruid), Michael E.
APPLICANT: Gruid), Michael E.
TITLE OF INVENTION: No. 6410221el Entomopoxvirus Expression System
FILE REFERENCE: UF114.C4.D1
CURRENT APPLICATION NUMBER: US/09/370,861A
CURRENT FILING DATE: 1990-08-09
PRIOR RAPLICATION NUMBER: US 07/991,867
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR APPLICATION NUMBER: US 08/107,755
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1992-02-12
PRIOR FILING DATE: 1992-01-13
PRIOR FILING DATE: 1991-02-19
PRIOR FILING DATE: 1991-02-19
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn version 3.1
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Pred. No. 0.17;
0; Mismatches 282; Indels 1
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US-09-370-861A-8
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Patent No. 6106825
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Best Local Similarity 44.4%;
Matches 226; Conservative
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4363 TATATATTTCAAATTTAAATATTATATTTAAATTTATAACAAATTAAAATATAA 4422
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                    429 CTCAAAAATAGTTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGGTCGGTTTC 488
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                                                                                                                                                                                                                                                                                                                  APPLICANT: MOYER, Richard W
APPLICANT: Li, Yi
APPLICANT: Hall, Richard L
APPLICANT: Hall, Richard L
TITLE OF INVENTION: ENTOWOPOXVIRUS-VERTEBRATE GENE DELIVERY
TITLE OF INVENTION: VECTOR AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.1%; Score 45.8; DB 3; Length 4 ilarity 44.4%; Pred. No. 0.22; Conservative 0; Mismatches 282; Indels
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APPLICATION NUMBER: US/08/852,629
                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: Florida
                                                                                                                                                4635 TAGAAAATTAATTAATTTAAAAAATTA 4663
                                                                                                         489 GTAAAAAAAAAAAAATTTAAAAAATATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35,746
FR: UF-184
                                                                                                                                                                                                                                                       Sequence 15, Application US/08852629 Patent No. 6106825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF-1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4838 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 407-839-8589
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     407-839-8589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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Matches 226; Conserv
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4395 CATATTTAGATATATCTTATAACAAAAATAGCAATATAAGTAATATTTATACTACCACATT 4454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 CCGGGGTCTGTACTATGGCAAGATACTATTCTACCACTAGACCATTGGTTCATTTTGTTT
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APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Li, Yi
APPLICANT: Hall, Richard L
TITLE OF INVENTION: ENTOMOPOXVIRUS-VERTEBRATE GENE DELIVERY
TITLE OF INVENTION: ENTOMOPOXVIRUS-VERTEBRATE GENE DELIVERY
TITLE OF INVENTION: LOYOR AND METHOD
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: Saliwanchik, Lloyd & Saliwanchik
STREET: Gainesville
STATE: Florida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 45.8; DB 3; Length 4810;
Pred. No. 0.22;
0; Mismatches 282; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING_DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Bencen, Gerard H
REGISTRATION NUMBER: 35,746
REFRENCE/DOCKET NUMBER: UF-16
TELEPHONE: 407-426-7500
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 400-839-8589
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 4810 base pairs
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                                                                                                                                                                                                                                                                                                    ZIP: 32606
COMPUTER READABLE FORM:
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STRANDEDNESS: both
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Best Local Similarity
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MOLECULE TYPE: CD
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ANTI-SENSE: NO
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Matches
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APPLICANT: DISK, Alexander
APPLICANT: DISEK, Alexander
APPLICANT: DISERBROCK, Christian
APPLICANT: DISEBREACK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: Dy Assessing DNA Methylation
TITLE OF INVENTION: DAY Assessing DNA Methylation
TITLE OF INVENTION: DAY Assessing DNA Methylation
TITLE OF INVENTION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: DC7/FP01/03971
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10013259.7
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 28
LENGTH: 11131
                                                                                                                                                   4542
                                                                                                                                                                                                                                                    1543 TAGTAAATTTAAAAATTAATAATATCTAAAATAAATTGGTAACTTTAATAATGTTT 4602
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                                                4423 CATATTTAGATATATCTTATAACAAAAATAGCAATATAAGTAATATTATACTACCACATT 4482
                                                                                                                                                                                                                                                                                                                                                     1603 TICCTATTAGTATAGTTGAGTTAAATATGGAATCAATACAATAAAAGATTATAAATITA 4662
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249 CCAAAGTTGGTCGATTTTAAAAAGTAAAATTACTTACCAAAGTTGGTCGATTTTTT 308
                                                                                                                                                                                                    369 TATITIAATIGAAAACTAACCAAAGTTAGTCGGTTTCTTGAAACATAAATTTCGCGGGA 428
                                                                                                                                                                                                                                                                                                       429 CTCAAAAATAGTTTCCCGCATTTTTGCGCCAAAGAAAACCGACCAAAGTTGGTCGGTTTC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 TAAAAAGTAAAATTACTTACCAAAGTTGGTCGATTTTTTTAAATGATCCGCCGAATTAAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              725 TAAAACCGAAAATTCAAAACCAACCTAAACAACATAATAAAACTACGTCTCTACTAAAA 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  665 ATACAAAATTAACTAAAAATAATAACGAACGTCTATAATCCCAACTAATTAAAAAACTAA 606
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                                                                                                   1483 CTATAGAATTTTTAAATTGTGAATCATGTAATATAATGACTATAATTTTTATTAATAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.1%; Score 45.8; DB 4; Length 11131; Best Local Similarity 48.6%; Pred. No. 0.27; Matches 125; Conservative 0; Mismatches 132; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                      1663 TAGAAATTAATTTAATTTA 4691
                                                                                                                                                                                                                                                                                                                                                                                                        489 GTAAAAAAATTTAAAAATATATA 517
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Sequence:

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APPLICANT: Chromagenics B.V.
APPLICANT: Ctromagenics B.V.
APPLICANT: Ctromagenics B.V.
APPLICANT: Ctrokeberg, Arthur D.
APPLICANT: Kruckeberg, Arthur D.
TITLE OF INVENTION: DMA sequences comprising gene transcription regulatory qualities & TITLE OF INVENTION: DMA sequences
CURRENT APPLICATION NUMBER: US.10/190,312A
CURRENT FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: 60/303,199
PRIOR RILING DATE: 2001-07-05
NUMBER OF SEQ ID NOS: 1079
SOFTWARE: Patentin version 3.1
SEQ ID NO 97.
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Pred. No. 0.0011;
0; Mismatches 72; Indels 0;
                                                                                                     US-03-92-05-22.
US-10-221-455-559
US-10-239-676-96
US-10-239-676-96
US-10-239-676-96
US-10-239-676-96
US-10-239-676-96
US-10-021-323-16830
US-10-021-323-16830
US-10-021-323-7699
US-10-0311-455-1598
US-10-311-455-1598
US-10-311-455-952
US-10-311-455-3080
US-09-790-988-1
                      6 US-10-221-613-36
5 US-10-311-455-757
6 US-10-221-613-137
7 US-10-021-323-7699
7 US-10-021-323-17801
US-09-960-352-11234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: sequence of STAR A13
US-10-190-312A-97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 97, Application US/10190312A Publication No. US20030199468A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                        7.2%;
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469
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3673778
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Best Local Similarity 60.0°
Matches 108; Conservative
             368
6092
8979
8979
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396
11914
15732
115732
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499
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 US-10-190-312A-97/c
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80400
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                                                                                               November 11, 2004, 10:27:15; Search time 482.239 Seconds (without alignments) 10091.039 Million cell updates/sec
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Published Applications Nat.

(ggn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

(ggn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*

(ggn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*

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(ggn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

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(ggn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

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(ggn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*

(ggn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

(ggn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-190-312A-119
6 US-10-424-599-109423
5 US-10-311-455-28
5 US-10-311-455-2145
6 US-10-240-485-177
US-09-887-576-129
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S US-10-312-841-1
US-10-021-323-93
US-10-311-455-1749
US-10-240-453-171
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                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications NA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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Match Length DB
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Sequence 2, Appil Sequence 1491, Ap Sequence 13802, Ap Sequence 10189, Ap Sequence 2074, Ap Sequence 2940, Ap Sequence 1220, App Sequence 11, App Sequence 1, Appl Sequence 206, App Sequence 206, App Sequence 206, App Sequence 306, App Sequence 306, App Sequence 2080, App Sequence 1369, App

Minimum DB Maximum DB

Database

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APPLICANT: OLEK, ALEXANDER
APPLICANT: PIPENBROCK, Christian
APPLICANT: PIPENBROCK, Christian
APPLICANT: PIPENBROCK, Christian
APPLICANT: BERLIN, Kur.
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determil
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: cytosine methylation
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE 1002-12-16
PRIOR FILING DATE: 2001-07-02
PRIOR FILING DATE: 2001-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NOS: 2424
                                                                                                                             1936 ITAAATTAAATGCACCAGCGGGAATCGAACCCGGGTCTGTACCGTGGCAGGGTAT 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 ATTAIGIAATAAAAAGAITCACTAICTGGGAATCGAACCGGGGTCTGTACTAIGGCAAGA
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US-10-311-455-58
                                                                                                                                                                                    158 ICTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTT 206
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Pred, No. 0.0018;
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Similarity 45.7%; Pred. No. 0.0029;
23; Conservative 0; Mismatches 265; Indels
                                                                                                                                                                                                                                                                                                                                                     Sequence 58, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                             .;
                    74.38;
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                                               81; Conservative
               Best Local Similarity
Matches 81; Conserv
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Best Local Simi
Matches 223;
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                                                                                                                                                                                                                Sequence 119, Application US/10190312A
; Sequence 119, Application US/20030199468A1
; Publication No. US20030199468A1
; Publication No. US20030199468A1
; GENERAL INFORMATION:
; APPLICANT: Chromagenics B.V.
; APPLICANT: Chromagenics B.V.
; APPLICANT: Chromagenics B.V.
; APPLICANT: Chromagenics B.V.
; TITLE OF INVENTION: DNA sequences comprising gene transcription regulatory qualities
; TITLE OF INVENTION: methods for detecting and using such DNA sequences
; TITLE OF INVENTION: WHERE: US/10/190,312A
; CURRENT APPLICATION NUMBER: US/10/205
; FRIOR FILING DATE: 2001-07-05
; WUMBER OF SEQ ID NOS: 1079
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 119
; SEQ ID NO 119
; TABOTH: 1140
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US-10-42-599-109423
Sequence 109422, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF UNVENTION DAMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DAME: 2003-04-28
SEQ ID NO 109423
LENGTH: 2131
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                         306 TCTACCACTAGACCACTGGTGCTTTTTTGATTAAACACGACTAAATATTAATATAGAT 247
                                                                      218 ITTAATTATTTTGCACGAAATAACCGACCAAAGTTGGTCGATTTTATTAAAAGTA
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_69823C.1
US-10-424-599-109423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 64.2;
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US-10-190-312A-119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 60.0%;
Matches 108; Conservative
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                                                                                                                                                                                                                  US-10-190-312A-119/c
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Pred. No. 0.0075;
0; Mismatches 267; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-485-177
                                                                                                                                                     Sequence 177, Application US/10240485

Publication No. US20030148327A1

GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007

CURRENT APPLICATION NUMBER: US/10/240,485

CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR PILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 202

SEQ ID NO 177

LENTH: 15518
  514 TATATTTAAAAACCGACCAA 535
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.6%;
Matches 234; Conservative
                                                                                                                                            -10-240-485-177/c
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APPLICANT: OLEK, Alexander
APPLICANT: DLEFENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: Cytosine methylation
FILE REFERENCE: 5013.101
FILE REFERENCE: 5013.101
FILE REFERENCE: 2001-0.02
FRICE REPERENCE: 2000-06-30
FRICE REPERENCE: 2000-06-30
FRICE REPERENCE: 2000-06-30
FRICE REPERENCE: 2000-06-30
FRICE REPERENCE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 2145
FUND THE PROOF FRICE REPERENCE: 2000-09-01
342 AACTACGAACCTAAAAAAAAAAAAAAAAACTTCAAAATTCTATTATAAAATTTTTCTTT 883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 CTATTCTACCACTAGACCATTGGTTCATTTTGTTTTAAGACTGTCTTTTATTTGATTTAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                822 AAAAATAACTATTTAAAAATTAATACTAATACTCTCCATACTATTCTATATTCTTAAAAT 763
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Pred. No. 0.0075;
0; Mismatches 267; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-2145
                                                                                                                                                                                                                                                        US-10-311-455-2145/c
; Sequence 2145, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATATTTTAAAAACCGACCAA 535
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ORGANISM: Artificial Seguence
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Best Local Similarity 46.6%;
Matches 234; Conservative
                                                                                                                                         5060 ATCAAATT 5053
                                                                                   512 AATATATT 519
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2573915 AAAAITTITCAATCAICTAATITIACAITTIATACTACCICCCAAAAITTITITITAAICA 2573856
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                                       1593577 Gregrarrriarriarrieigriririercearricerririgereirrrarriarririreer 1593636
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44 AAAAAAATATTGTAAAAAAAAAACCGACCAAAGTTGATCGGTATTTTAATTATGTAATAA 103
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                                                                               AAAGATTCACTATCTGGGAATCGAACCGGGGTCTGTACTATGGCAAGATACTATTCTACC
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                                                                                                                                                                                                                                                                                                                                     CITACCAAAGIIGGICGAIITITITAAAIGAICCGCCGAAIIAACCGACCAAITITGGIA
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US-10-312-841-1/c
Sequence 1, Application US/10312841
Publication No. US20030186277A1
GENERAL INFORMATION:
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Matches 223; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ) NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1
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Publication No. US20030186277A1

GENERAL INFORMATION:
APPLICANT: Epigenomics AG

TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHG

FILE REFERENCE: B01/1208/WO

CURRENT APPLICATION NUMBER: US/10/312,841

CURRENT FILING DATE: 2002-12-30

NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                       APPLICANT: Brown, D.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Chang, H.
APPLICANT: Ann, B.
APPLICANT: Ann, B.
APPLICANT: Wang, X.
APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
FILE REFERENCE: 1360,0011831
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR PLILING DATE: 2000-06-25
PRIOR PLILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-10-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 129
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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6.4%; Score 58; DB 15; Length 36
Best Local Similarity 47.1%; Pred. No. 0.61;
Matches 178; Conservative 0; Mismatches 200; Indels
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  Sequence 129, Application US/09887576
Patent No. US20020144047A1
GENERAL INFORMATION:
APPLICANT: Budworth, P.
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US-09-887-576-129
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ORGANISM: Artificial Sequence
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; LOCATION: (3294164)
US-10-312-841-1
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LENGTH: 3673778
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APPLICANT: OLEX, Alexander

APPLICANT: OLEX, Alexander

APPLICANT: PIEDENBROCK, Christian
TITLE OF INVENTION: Cytosine methylation
FILE OF INVENTION: Ottosine methylation
FILE REFERENCE: 5013.1014
CURRENT FILING DATE: 2002-12-16
FRIOR APPLICATION NUMBER: DC12-16
FRIOR APPLICATION NUMBER: DE 10032529.7
FRIOR PRING DATE: 2000-06-30
FRIOR FILING DATE: 2000-06-30
FRIOR APPLICATION NUMBER: DE 10043826.1
FRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1749
LENOTH 6339
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172 ATTGGTTCATTTTAAGACTGTCTTTTATTTGATTTATACTCTTTAATTATATTT
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Pred. No. 0.19;
0; Mismatches 196; Indels
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                                                                                                                                                                                                                                                    ; Sequence 1749, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 46.9%;
Matches 173; Conservative
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                                                                                                                                                                                                                                    Sequence 93, Application US/10021323
Publication No US20040123340A1
APPLICANT: Delkman, Jill
APPLICANT: Feng, Paul C.C.
APPLICANT: Feng, Faul C.C.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Karen L.
APPLICANT: Fincher, Paul C.C.
APPLICANT: Fincher, Bull C.C.
APPLICANT: Jille OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5.274)8
CURRENT APPLICATION NUMBER: US/10/021,323
CURRENT FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 60/255, 619
NUMBER OF SEQ ID NOS: 17880
  2573795 ТІТІТІАТІТАААДІАТІТІТІАДІАГАГАГАГІТТАТІАТАТА ГАГАГАГАГАТАТАТАТАТАТ
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Pred. No. 0.052;
0; Mismatches 249; Indels
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LOCATION: (1)..(552)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: LIB325-001-Q1-K6-C5
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Best Local Similarity 44.8%;
Matches 202; Conservative
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ORGANISM: Gossypium hirsutum
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US-10-021-323-93/c
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APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determiting Corp. Invention: Cytosine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: US/20/07537
PRIOR PAPLICATION NUMBER: DE 10032529.7
PRIOR PILING DATE: 2001-07-02
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
NUMBER: OF SEQ ID NOS: 2424
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Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown, Jeffrey
APPLICANT: Brown Over Genes
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
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TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: OF HUMAN CANCERS
TITLE OF INVENTION: AND THERAPY
TITLE OF INVENTION NUMBER: US/09/834,975
CURRENT APPLICATION NUMBER: 00/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SEQ ID NO 47
LENGRAPH: 368
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Best Local Similarity 47.6%; Pred. No. 0.2;
Matches 162; Conservative 0; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA

TITLE OF INVENTION: Transcription

TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated

TITLE OF INVENTION: With DNA TRANScription

FILE REFERENCE: 5013.1009

CURRENT APPLICATION NUMBER: US/10/240,453

PRIOR APPLICATION NUMBER: PCT/EP01/03973

PRIOR FILING DATE: 2001-04-06
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                                                        Sequence 171, Application US/1024045
Publication No. US20030148326A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
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ORGANISM: Artificial Sequence
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Best Local Similarity 46.9
Matches 173; Conservative
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| Sequence 36, Application US/10221613 |
| Publication No. US2004002912341 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| APPLICANT: PIBEBNBROCK, Christian |
| APPLICANT: BERLIN, Kurt |
| TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle |
| FILE REFERENCE: 5013.1004 |
| CURRENT FILING DATE: 2002-09-13 |
| PRIOR APPLICATION NUMBER: US/10/221,613 |
| CURRENT FILING DATE: 2002-09-13 |
| PRIOR PILING DATE: 2001-03-15 |
| DE 10019058.8 |
| DE 1001913.8 |
| DE 10043826.1 |
| PRIOR FILING DATE: 2001-03-15 |
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-613-36
                                                                                                                                                                                       Query Match 6.1%; Score 54.6; DB 9; Length 368; Best Local Similarity 44.2%; Pred. No. 0.096; Matches 138; Conservative 0; Mismatches 174; Indels
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NAME/KEY: misc_feature
| LOCATION: (1)...(368)
| OTHER INFORMATION: n = A,T,C or
US-02-834-975-47
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2000-09-01
; NUMBER OF SEQ ID NOS: 428
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: November 11, 2004, 06:56:19; Search time 4307.14 Seconds (without alignments) 10990.348 Million cell updates/sec 1001 Sequence: 1 aatatagacttttgattaaaacccactactagaaatccgg 1001 Scoring table: Scoring table: Searched: 4526729 seqs, 23644849745 residues Total number of hits satisfying chosen parameters: Minimum DB seq length: 2000000000 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 100% Listing first 45 summaries	## 1 1 1 1 1 1 1 1 1 1

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PAT 19-JAN-2001 linear

DNA

3294 bp. Sequence 1 from Patent W00077187. AX068012. GI:12329820

RESULT 2
AX068012
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KEYWORDS
SOURCE
ORGANISM

Nicotiana tabacum (common tobacco)
Nicotiana tabacum
Nicotiana, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Nicotiana.

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

Promoter system and production and use of the same Patent: WO 0077187.A 1.21-DEC-2000; Roitsch, Thomas, Dr. (UB) Location/Qualifiers Roitsch, T. D. Promoter sys

2037

1. .3294 -/organism="Nicotiana tabacum" /mol_type="unassigned DNA" /db_xref="taxon:4097" source

0

1196 1316 1256 1376 1436 1736 1496 1556 1616 1676 1796 1856 1916 2036 240 960 120 180 300 360 420 480 540 099 720 840 900 009 780 9 1197 GATAATAACTICAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAG 1377 TGAGGTGGATGATTCTTTTTTGACAATGATGAATGATGGNCAAATACTAGAATGTTGG 1797 TTAATGAAAGCAGATTTTGACCATACAATAATATGACAAAATTGCTTCCAAAGAAAACA GATAATAACTTCAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAG 1317 CAATAAATAACGATAAATGGCATTAAAGTAAATAAGGAGAAATGATTCACCCAATATTGAA 361 AGGTAGTGATTGTCTTTTATCTAGAGAGAAAGTCTGCTTTTCAAAGAATATTTTTATCAG 1557 AGAATATTACATCCCCCTCTCTCCCCTATNICTTTTTTTATATGGGACATTCCTCAA 1617 TCAATCCTAAAAGTACATACACCAAGAATATTCAATAAAATATTTTTTTGAATATTTCTAT 1677 TATAAAAACTAGCTGTTAGCACTCGACCTCGGCGCGTCGNTATTGACTACTCGGTTACGAGCCC 1)37 IGICALTIACIAATGGACCTGGATIACATCACTITCTACGAIACTGCTTCATGTCAATC CITAGTAACTATATATCAAAGGAATGGTITTTTTCTTTAAATATGGATAAAATTTGTG AATATAGAAGATTAGATTAACAAAGGTTATGGTGGAGTGGTAAGCAGAGGCGGACC 1 AATATAGACTTTTGATTAAATTAATTAATATTGTATGACAAAGGATTAAACCTAGTTAAT 1137 AATATAGACTITIGATTAAATTAATTATTGTATGACAAAGGATTAAACCTAGTTAAT AAGATTAAATGTGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGAATATCAAG CAATAAATAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAA TGAGGTGGATGTTCTTTTTTTTGACAATGATGAATGGCGCAAATACTAGAATGTTGG GACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAGAAAATCTCTTTAGAA 1497 AGGTAGTGATTGTCTTTTATCTAGAGAGAAAGTCTGCTTTTCAAAGAATATTTTTATCAG 421 AGAATATTACATCCCCCTCTCCCTATCTCTTTTTCTATTATATGGGACATTCCTCAA TCAATCCTAAAAGTACATACACCAAGAATATTCAATAAAAATATTTTTTTGAATATTCTAT TGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATC TTAATGAAAGCAGATTTTTGACCCATACAATAATATGACAAAAATTGCTTCCAAAGAAAACA TGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGA ATAGEGITITITICITITICATATCATATCAGAGIAAAGCAACCATGAATAGAAAAGG CITAGTAACTATATATACAAAGGAATGGTGTTTTTTTCTTTAAATATGGATAAAATTTGTG TATAAAAACTAGCTGTTAGCACTCGACTCGGTCGYTATTGACTACTCGGTTACGAGCCC Gaps ö Length 3294; Query Match
99.6%; Score 997; DB 6; Length 32
Best Local Similarity 99.6%; Pred. No. 3e-171;
Matches 997; Conservative 0; Mismatches 4; Indels 61 181 241 481 541 199 121 721 301 601 781 841 1977 901 ORIGIN à В ò g ò d ò ద ò g ò 엄 δ g ò d ö g ò g à qq ò 8 8 8 à q $\stackrel{>}{\circ}$ g ò

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1 (bases 1 to 3293)
Godtz, M., Godt, D.E., Guivarc'h, A., Kahmann, U., Chriqui, D. and
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University of Regensburg, Universitaetsstr. 31, Regensburg 93053,
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Induction of male sterility in plants by metabolic engineering
the carbohydrate supply
Proc. Natl. Acad. Sci. U.S.A. (2001) In press
2 (bases 1 to 3293)
Goetz,M., Godt, D.E. and Roitsch, T.
Direct Submission
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                          2097 TATGTGTTATAGTAAGGGGTCACCCACTACTAGAAATCCGG 2137
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light harvesting chlorophyll
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Nicotiana sylvestris (wood tobacco)
Nicotiana sylvestris
Nicotiana sylvestris
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                            encoding
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Organization and transcription of the gene family encodir
chlorophyll a/b-binding proteins in Nicotiana sylvestris
Gene 289 (1-2), 161-168 (2002)
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/db_xref="taxon:4096"
/clone="lambda NSCBel"
/tissue type="leaf"
/clone lib="lambda DASH genomic library"
2242.
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Hasegawa, K., Yukawa, Y., Sugita, M. and Sugiura, M.
Direct Submission
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                                                                               AB012639 3663 bp DNA Nicotiana sylvestris Lhcb1*7 gene for la/b-binding protein, complete cds.
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/product="light harvesting
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/gene="Lhcb1*7"
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/gene="Lhcb1*7"
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                                      Score 980.6; DB 8;
Pred. No. 2.9e-168;
                                                                                   'n,
                                                                                 1; Mismatches
                                      98.0%;
                                                             Best Local Similarity 99.3
Matches 994; Conservative
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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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5777: gap of 100 bp
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18208: gap of 100 bp
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21619. .64982.
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                              1855 TGGTAACACATGATAAATGTTCTGGAAAATCAGGAATAGTAATGTAGCATATAATATTCC 1796
                                                                                                                                                                                                 795 TIGAACAACAATAAATGATATTTGATTAATAGGAGGAATGATTCTTTTAATAAAGGGTA 1736
                                                                                                                                                                                                                                                                                                1735 GAATAAATGAACCTTCCACCTGACCATGAT---TGATAGACAAATCCTCGAATGATCGAG 1679
                                                                                                                                                                                                                                                                                                                                                                                     1678 GATTTCTCGGATCT-----GATGGTAAGTGTAGACAAAATTTCTGTGAAAA 1630
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                                                                                                                                                                                                                                                     243 AGGIGGAIGCIICTITITGACAAIGAIGAAGGCCAAAIACTAGAAGGAATGTIGGGA 302
                                                                                                                                                                                                                                                                                                                                             303 CCCTTCTCGGATCTAATGAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                    363 GTAGTGATTGTCTTTTATCTAGAGAGAAGTCTGCTTTTCAAAGAATATTTTTATCAGAG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           479 AATCAATCCTAAAAGTACATACAACAAGAATATTCAATAAAATATTTTTTGAATATTCT 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (11-AUG-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:
cfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 164256)
                                                                                                                                                                  183 ATAAATAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATG
                                                                         127 AAATGTGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGA----ATATCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: XGAP4, version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 158159 bases at least Q40
Consensus quality: 159450 bases at least Q30
Consensus quality: 160402 bases at least Q30
Insert size: 162956; sum-of-contigs
Insert size: 176864; z.6% error; agarose-fp
Quality coverage: 5.86x in Q20 bases; sum-of-contigs Quality
coverage: 5.66x in Q20 bases; sum-of-contigs Quality
  Center: Wellcome Trust Sanger Institute
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Web site: http://www.sanger.ac.uk
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HTG; HTGS PHASE1; HTGS DRAFT.
Danio rerIo (2ebrafish)
Danio rerio
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Direct Submission
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VERSION
KEYWORDS
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AUTHORS
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JOURNAL
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CR678065
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Direct Submission

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

Cambridgeshire, CB10 15A, UK. E-mail enquiries:

On Apr 19, 2002 this sequence version replaced gi:20145317.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either dunble-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and respeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was contirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em. EMBL; $x; $NISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at

Chromosome 13, constructed by the Sanger Centre Chromosome 13

Mapping Group. Purther information can be found at

http://www.sanger.ac.uk/HGPChr13

XXyac-R12G2: si from the IDI Human YAC library (RA) VECTOR: pYAC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:9606"
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  TITLE
JOURNAL
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                                                                                                                                                                                                             Score 66.6; DB 2; Length 164256; Pred. No. 0.007;
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                                                          /note="assembly_fragment:00059"
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135777. .138672
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                                                                                           Length 79018;
                                                                                           tch al Similarity 43.2%; Pred. No. 0.012; Pred. Yol; Conservative 2; Mismatches 521; Indels
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/clone="XXyac-R12DG2"
/clone_lib="ICI_YAC_RA"
                                                                                                Query Match
Best Local Similarity
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PRI 19-APR-2002

Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

AL627107.32 GI:20218583

sapiens (human)

Homo

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

Phillimore, B

REFERENCE AUTHORS

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                                                                                                                                                                                                                                                                                                71248 АТАААТАТАТАТАТАТАТАТАТАТА ТАЧААĞ ҚАТАТАТАТАТАТАТА Қ
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                                                                                                                                                                                                                                                                                                                                                                                                                  845
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Submitted (23-JAN-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Jan 25, 2004 this sequence version replaced gi:41223804.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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                                                                                                       AAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCA
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Insert size: 192554; 9.5% error; agarose-fp
Quality coverage: 8.71x in Q20 bases; sum-of-contigs Quality
coverage: 9.44x in Q20 bases; agarose-fp
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 20460i bases at least Q40
Consensus quality: 205156 bases at least Q20
Consensus quality: 20558 bases at least Q20
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HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
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Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        933
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Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 207772)
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Gaps

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runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of 100 bp
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contig of 64481 bp in length
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contig of 2378 bp in length
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contig of 1310 bp in length
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/clone="DKEY-1416"
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Danio rerio clone DKEY-1416, *** SEQUENCING IN PROGRESS ***, 11

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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 201329)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 198670 bases at least Q40
Consensus quality: 198670 bases at least Q30
Consensus quality: 199214 bases at least Q30
Insert size: 2010329; sum-of-contigs
Insert size: 191135; 3.8% error; agarose-fp
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HTG; HTGS PHASE1.
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                                                 Gaps
Query Match
Best Local Similarity 38.8%; Pred. No. 0.018;
Matches 262; Conservative 1; Mismatches 410; Indels 3;
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Chemistry: Dye-terminator; 100% of reads
Consensus quality: 153457 bases at least Q40
Consensus quality: 153769 bases at least Q30
Consensus quality: 154184 bases at least Q20
Insert size: 155463; sum-of-contigs
Insert size: 154616; 5.6% error; agarose-fp
Quality coverage: 7.69x in Q20 bases; sum-of-contigs Quality
coverage: 7.75x in Q20 bases; agarose-fp
                                                                                                                                                                                 * NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the apps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                               42348: contig of 42348 bp in length 42448: gap of 100 bp 56828: contig of 14380 bp in length 56928: gap of 100 bp 69959: contig of 13031 bp in length 70659: gap of 100 bp in length 74154: contig of 4095 bp in length 74254: gap of 100 bp in length 83830: gap of 100 bp in length 83830: gap of 100 bp in length 111539: contig of 27709 bp in length 111639: contig of 100 bp in length 13084: contig of 18445 bp in length 130184: gap of 100 bp
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'ragment_chain:2"
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ragment_chain:2"
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fragment chain:2"
138234. 146836
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/note="assembly_fragment:00607
fragment_chain:1"
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fragment_chain:2"
83831. .111539
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:ragment_chain:2"
:30185. __138133
Assembly program: XGAP4; version 4.5
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4255. .83730
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*** SEQUENCING IN PROGRESS ***, 11
                                                                                                                                                                                   AAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCA 605
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                                                                                                                                           606 TTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATCTTAAT
                     ttctcggatctaatgaaaaagtatggaatagtagataatcgaatctctttagaaaggta
                                                                                                    366 GTGATTGTCTTTTATCTAGAGAGAAAGTCTGCTTTTCAAAGAATATTTTTATCAGAGAAT
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Center: Wellcome Trust Sanger Institute
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unordered pieces.
CR388010
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HTG; HTGS PHASE1.
Danio rerio (zebrafish)
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                                                                                                                                                                                                                                                                                          578
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Actinopterygii, Neopterygii; Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.
1 (bases 1 to 160534)
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cfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                          AATATTTTTTTGAATATTCTATTATAAAACTAGCTGTTAGCACTCGACCTCGGTCGYTA
                                                                                                                                                                                                                           639 CGATACTGCTTCATGTCAAATCTTAATGAAAGCAGATTTTGACCCATACAATAATATGAC
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                                                                                                                                                           6.4%; Score 64; DB 2; Length 156463;
llarity 47.2%; Pred. No. 0.021;
Conservative 1; Mismatches 246; Indels 1
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/note="assembly_fragment:00168
fragment_chain:2"
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/note="assembly_fragment:00105.0"
151822..156463
/note="assembly_fragment:00049
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Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
Project Information
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vector_side:right"
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HTG; HTGS PHASE1.
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Danio rerio (zebrafish)
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Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 157308 bases at least Q40
Consensus quality: 157308 bases at least Q30
Consensus quality: 157864 bases at least Q20
Insert size: 159634; sum-of-contigs
Insert size: 176376; 2.7% error; agarose-fp
Quality coverage: 8.20x in Q20 bases; sum-of-contigs Quality
coverage: 7.72x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                               * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9994: contig of 8994 bp in length 9094: gap of 100 bp 31712: contig of 22618 bp in length 31812: gap of 100 bp 50359: contig of 18547 bp in length 50459: gap of 100 bp 56678: gap of 100 bp 61866: contig of 6119 bp in length 56678: gap of 100 bp 61866: gap of 100 bp 61866: gap of 100 bp 89946: gap of 100 bp 89946: gap of 100 bp 130975: contig of 41129 bp in length 130975: contig of 41129 bp in length 13075: gap of 100 bp 143529: contig of 12454 bp in length 143529: contig of 4435 bp in length 14864: gap of 100 bp 14864: gap of 100 bp 14864: gap of 100 bp 14864: gap of 100 bp 14864: gap of 100 bp 16654: contig of 12370 bp in length 16654: contig of 12370 bp in length 16654: contig of 12370 bp in length
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131076. 143529
/note="assembly_fragment:00557
fragment_chain:3"
143630. 148064
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1. 8994
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7. 00c="assembly_fragment:01004
fragment chain:1"
31813. 50359
7. 00c="assembly fragment:01306
fragment chain:1"
clone end:77
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conto. Escription
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fragment_chain:1"
56679. .. 61866
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note="assembly fragment:00715
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Center project name: L7524
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HOMO sapiens chromosome 4 clone RP11-775M3 map 4, WORKING DRAFT
ACGF790n
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                                                                                                                                                                                                                                                         373 TCTTTTATCTAGAGAGAAGTCTGCTTTTCAAAGAATATTTTTATCAGAGAATATTACAT 432
                                                                                                                                                                                                                                                                                                                                                                                                                                  493 GTACATACACCAAGAATATTCAATAAAATATTTTTTTTGAATATTTCTATTATAAAAACTAG 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       553 CTGTT---AGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCATTTA 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGAATAGTGTTT 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATATATCAAAGGAATGGTGTTTTTTTTTTAAATATGGATAAAAATTTGTGAATATAGAA 909
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens chromosome 4, clone RP11-775M3
                                                                                                                                                                       313 ATCTAATGAAAAAGTATGGAATAGTAATAATCGAATCTCTTTAGAAAGGTAGTGATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              670 GCAGATTTTGACCCATACAATAATATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTA
                                                                                                                                                                                                                                                                                                                                           610 CTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATCTTAATGAAA
                                                                                                                             Gaps
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                                                                                Score 64, DB 2; Length 160534;
Pred. No. 0.021;
0; Mismatches 401; Indels 3;
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Homo sapiens (human)
                  /note="assembly_fragment:00424"
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  148165. .160534
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                                                                                  Query Match
Best Local Similarity 34.7%;
Matches 215; Conservative
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Direct Submission

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 201312)

Research, 320 Charles Street, Cambridge, MA 02141, USA

CE 3 (bases 1 to 201312)

RES BITTEN, B. Linton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Callymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Ginde, S., Goyette, M., Graham, L., Garad-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illiev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Hagos, B., Macthews, C., Macthews, C., Macdonald, P., McKernan, K., Marquis, N., Matthews, C., McCarthy, M., McEwan, C., Macdonald, P., Marguis, N., Matthews, C., McCarthy, M., McEwan, C., Macdonald, P., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Santos, R., Santos, R., Santos, R., Santos, R., Santos, R., Santos, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Schupback, R., Velman, D., Ye, W. J., Young, G., Zalnoun, J., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zalnoun, J., Kesearch, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker:

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                            Collymore, M., Cooke, P., Deverlano, K., Dewarr K., Diaz, J. S., Cooke, P., Deverlano, K., Dewarr K., Diaz, J. S., Cooke, P., Deverlano, K., Dewarr K., Diaz, J. S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Garchere, M., Garham, L., Grand, P., Garen, C., Kann, L., Karatas, K., Handos, B., Landors, T., Lehoczky, J., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPeeters, R., Meldrim, J., Mencus, L., Mihova, T., Miranda, C., Minenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Connoll, P., O'Neil, D., Olivar, T.W., Oliver, J., Peterson, K., Pierre, N., Santos, R., Schauer, S., Severy, P., Spencer, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vasiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Wyman, D., Ye, W.J., Young, G., Subrission, M., Zimmer, A. and Zody, M., Myman, D., Ye, W.J., Direct, Subnission
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Center: Whitehead Institute/ MIT Center for Genome Research
Choepel,Y., Colangelo,M., Collins,S.,
Arellano,K., Dewar,K., Diaz,J.S.,
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Insert size: 200912; sum-of-contrigs
Quality coverage: 9.1 in Q20 bases; agarose-fp
Quality coverage: 9.5 in Q20 bases; agarose-fp
Quality coverage: 9.5 in Q20 ba.
NOTE: This is a 'working draft' sequence. It currently
consists of 5 contrigs. The true order of the pieces
is not known and their order in this sequence record is
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Web site: http://www-seq.wi.mit.edu
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CR354440 154675 bp DNA linear HTG 27-MAR-2004
Danio rerio clone DKEYP-100B9, *** SEQUENCING IN PROGRESS ***, 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                 TGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATC
                                                                                                                                                                                                             TTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAATTGCTTCCAAAGAAAACA
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Insert size: 163247; 2.2% error; agarose-fp
Quality coverage: 8.23x in Q20 bases; sum-of-contigs Quality
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Danio rerio (zebrafish)
Danio rerio
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CR354440
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                                                                                   1 77871: contig of 77871 bp in length 77872 77971: gap of 100 bp 10159: contig of 5188 bp in length 1160 81259: gap of 100 bp 100 bp 115560: contig of 32201 bp in length 115560: gap of 100 bp 100 bp 1561 158995: contig of 43435 bp in length 1996 201312: contig of 42217 bp in length 10056 201312: contig of 42217 bp in length.
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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Nicotiana sylvestris DNA flanking T-DNA insert line S22KdotNOSpro
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Nicotiana sylvestris
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots;
asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   493 GTACATACACCAAGAATATTCAATAAAATATTTTTTTG-AATATTCTATTATAAAAACTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 ATCTAATGAAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGGTAGTAGTTG
                                                                                                                                                                                                                                                                                                                      612 AATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATCTTAATGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 TCTTTTATCTAGAGAGAAAGTCTGCTTTTTCAAAGAATATTTTTATCAGAGAATATTACAT
                                                                                                                                                                                                                                                                                                                                                                                      552 GCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCATTTACT
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                                                                7;
6.3%; Score 63; DB 2; Length 154675;
larity 39.0%; Pred. No. 0.032;
Conservative 0; Mismatches 340; Indels 1
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variation annotation may not be found in the sequence submission corresponding to the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNDEP; Information on the WORNDEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human echromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group, Further information, can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
                                                                                                                                                                                                                                                                                                                                                                                                           constructed by the group
                         On Mar 23, 2003 this sequence version replaced gi:18476714.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
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RP11-269F19 is from the library RPCI-11.1 c
of Plater de Jong. For further details see
http://www.chori.org/bacpac/home.htm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: humquery@sanger.ac.uk
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Catarrhini, Hominidae, Homo.
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Direct Submission
Submitted (23-MAR-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2240 ATAMATICCTAGATAMAMACTGGGGTATGTCAGCGATATAAGACCGTGTTCAATGATGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                          Submitted (11-JAN-2001) Winden, van der J., Plant Molecular Genetics, Institute Of Molecular Biology, billrothstrasse 11, A-5020 Salzburg, AUSTRIA
Location/Qualifiers
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Human DNA sequence from clone RPI1-269F19 on chromosome
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Pred, No. 0.072;
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                                                                                                                                                                 /organism="Nicotiana sylvestris"
/mol_type="genomic DNA"
/db_xref="taxon:4096"
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Mammalia, Butheria, Primates,
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       Winden and van der,J.
Direct Submission
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22222222222222222222222222222222222222	AAF25736 standard; I AAF25736 standard; I AAF25736; 06-APR-2001 (first Tobacco invertase pi Tobacco; tapetum-spe male-sterile plant; transgenic plant; di Nicotiana tabacum. WO200077187-A2. 21-DEC-2000; 21-DEC-2000; 21-DEC-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 26-APR-2000; 2000DBB. 27-APR-2000; 2000BB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR-2000; 2000BBB. 27-APR
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plants of (e); (g) hybrid seed produced by crossing a male sterile plant of (e); (h) production of male sterile plants by introducing (II) into a cell and regeneration to a plant; (i) restorer plants contening in one (or preferably many) cells a construct (IIa) of (I) and a sequence that cencedes an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa); (k) seeds from plants of (e) (i) and (j); and (m) method for cloning a promoter that is functionally homologous with (I) constructs containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a heterologous invertase-encoding sequence are used to produce the retrologous invertase-encoding sequence are used to propare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) (I) can also be used to prepare transgenic plants that show increased or proteins involved in provision of energy to developing tissue. (I) provide high level expression in a tissue- and time-specific manner, and the new plants (e) developing tissue. (I) contrains involved in provision of energy to developing tissue. (I) contrains involved in provision of energy to developing tissue. (I) contrains involved in provision of energy to developing tissue. (I) contrains involved in provision of energy to developing tissue. (I) contrains the require expension in a tissue- and time-specific manner, and the contrains involved in provision of energy to developing tissue. (I)

Sequence 4312 BP; 1196 A; 827 C; 905 G; 1382 T; 0 U; 2 Other;

ö 2214 2274 2334 2394 2395 TGAGGGGGATGATTCTTTTTGACAATGATGAAAGGGGCAAATACTAGAATGTTGG 2454 2455 GACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAGTAGTAATCGAATCTCTTTAGAA 2514 2574 2575 AGAATATTACATCCCCCTCTCTCCCTATCTCTTTTTTCTATTTATATGGGACATTCCTCAA 2634 2754 240 120 600 121 AAGATTAAATGTGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGAATATCAAG 180 300 420 540 301 GACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAA 360 TGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATC 660 2215 GATAATAACTTCAGATCTATAATCAATTAACAGCAATCACGGTCATAGCGGTTGAGAG 2275 AAGATTAAATGTGGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGAATATACAAG 2515 AGGTAGTGTCTTTTATCTAGAGAGAAGTCTGCTTTTCAAAGATATTTTTATCAG 2695 TATAAAAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCC 2155 AATATAGACTTTTGATTAATTAATTAATTGTATGACAAAGGATTAAACCTAGTTAAT GATAATAACTTCAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAG 181 CAATAATTAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAA 2335 CAATAAATAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAA TGAGGTGGATGATTCTTCTTTTGACAATGATGAAGGATGGAGGCAAATACTAGAATGTTGG 361 AGGTAGTGATTGTCTTTTATCTAGAGAGAAAGTCTGCTTTTCAAAGAATATTTTATCAG TATAAAAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCC 1 AATATAGACTTTTGATTAAATTAATTAATTGTATGACAAAGGATTAAACCTAGTTAAT Gaps 99.9%; Score 1000.2; DB 4; Length 4312; 100.0%; Pred. No. 1.9e-198; tive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 1001; Conservative Similarity 241 541 Query Match 601 g g g g q QQ à à Ś ò ò à g d à g 8 QQ à \sim ፟

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2815 TTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAATTGCTTCCAAAGAAAAA 2874 2934 2994 CTTAGTAACTATATATCAAGGAATGGTGTTTTTTTTTTAAATATGGATAAAATTTGTG 3054 840 960 This invention describes a novel nucleic acid (I) comprising a promoter that is specific for tapetum and pollen. The invention also describes (a) expression system containing at least one (I); (b) nucleic acid construct (II) containing (I) plus at least part of an expressible nucleic acid distriction (II); (c) vector containing (I), the system of (a), or (II); (d) cells, particularly plant cells, containing (I), the system of (a), (II) or the vector of (c); (e) plants containing (I); the system of (a), (II) or the plants of (e); (f) production of male sterile plant of (f); (f) production of male sterile plants of (f); (f) production to a plant; (i) restorer plants containing in one (or preferably many) cells a construct (IIa) of (I) and a sequence that New tapetum- and pollen-specific promoter from tobacco, useful for preparing male sterile plants, particularly those with seedless fruits. Tobacco, tapetum-specific, pollen-specific, promoter; seed, invertase, male-sterile plant, in vitro embryogenesis, seedless fruit, transgenic plant, ds. 2875 TGGCTCTTATAGTGAAATATCGTTAGAACTGTTATAGAAAGATCTGAATTTATTATAAGA 841 CTTAGTAACTATATCAAAGGAATGGTGTTTTTTTTTTTAAATATGGATAAAATTTGTG AATATAGAAGATTAGATCAATTAACAAAGGTTATGGTGGAGTGGTAAGCAGAGGCGGACC TGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGA 3115 TATGTGTTATAGTAAGGGGTCACCCACTACTAGAAATCCGG 3155 TATGTGTTATAGTAAGGGGTCACCCACTACTAGAAATCCGG 1001 Tobacco invertase promoter SEQ ID NO 1. Claim 3; Page 64-65; 74pp; German. AAF25735 standard; DNA; 3294 BP 12-JUN-1999; 99DE-02009998. 04-APR-2000; 2000DE-02005992. 26-APR-2000; 2000DE-02007494. 13-JUN-2000; 2000WO-DE001944. 06-APR-2001 (first entry) WPI; 2001-080685/09. Nicotiana tabacum. (ROIT/) ROITSCH T. WO200077187-A2. 21-DEC-2000. Roitsch T; 661 721 781 2995 AAF25735; 901 961 AAF25735
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cencodes an invertase different from the plants endogenous invertase; (j)
plant that contains in one (or preferably many) cells both (II) and (Ia)
(i) kseeds from plants of (e), (i) and (j), and (m) method for
cloning a produced by plants of (e), (i) and (j), and (m) method for
cloning a promoter that is functionally homologous with (I). Constructs
containing (I) and an invertase-encoding sequence are used to produce
male-sterile plants (by co-suppression or antisense techniques) for
preparation of hybrids, while constructs that contain (I) and a
heterologous invertase-encoding sequence are used to prepare restorer
plants (which allow propagation of the male-sterile plants). Seeds from
these plants are used for in vitro embryogenesis of haploid or (double)
diploid plants, and the new plants particularly produce seedless fruits.

(I) can also be used to prepare transgenic plants that show increased or
reduced production of endogenous materials, e.g. of plant hormones or
provide high level expression in a tissue- and time-specific manner, and
contains involved in provision of energy to developing tissue. (I)
contains involved in provision of energy to developing tissue. (I)
contains the expense transgenic and time-specific manner, and
contains involved in the contain (e.g. temperature or chemicals) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 997; DB 4; I
Pred. No. 8.3e-198;
0; Mismatches 4;
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Matches 997; Conservative
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qq	1857 TGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGA 191
ò	781 ATAGTGTTTTTTTTTTTTTTTCAPATCTAAGGAGTAAAGGAACCATGAATAGAAAGG 840
Q	1917 ATAGTGTTTTTTTTTTTTTTTTTTTTAAGGAGTAAAGGAACCATGAATAGAAAAGG 197
λõ	CTTAGTAACTATATGAAAGGAATGGTGTTTTTCTTTAAATATGATAAAATTTGTG
d G	1977 CTTAGTAACTATATATCAAAGGAATGGTGTTTTTTTTTT
ර් සි	901 AATATAGAAGATTAGATCAATTAACAAAGGTTATGGTGGAGTGGTAAGCAGAGGGGGACC 960 2037 AATATAGAAGATTAGATCAATTAAACAAAGGTTTATGGTTGAGTGGAGTGGTAAGCAAGGGGGAAC 209
ŏ	961
q	2097 TATGTGTTATAGTAAGGGGTCACCCACTACTAGAAATCCGG 2137
RESU AAF2 ID	ILT 3 15742 AAF25742 standard; DNA; 4135 BP.
XX PC	NF25742;
XE	06-APR-2001 (first entry)
XE:	bacco promoter/ir
CE E E	Tobacco; tapetum-specific; pollen-specific; promoter; seed; invertase; male-sterile plant; in vitro embryogenesis; seedless fruit; transgenic plant; ds.
X 8	Nicotiana tabacum.
X E.	WO200077187-A2.
X C	21-DEC-2000.
4 g \$	13-JUN-2000; 2000WO-DE001944.
4 H H H	12-JUN-1999; 99DB-02009998. 04-APR-2000; 2000DE-02005992. 26-APR-2000; 2000DE-02007494.
XXI	(ROIT/) ROITSCH T.
X II S	Roitsch T;
% # \$	WPI; 2001-080685/09.
\ L L .	New tapetum- and pollen-specific promoter from tobacco, useful for preparing male sterile plants, particularly those with seedless fruits.
X & X	Example 4.3; Page 68-70; 74pp; German.
₹88	This invention describes a novel nucleic acid (I) comprising a promoter
88	that is specific for taperum and polien. The invention also describes (at expression system containing at least one (I); (b) nucleic acid construct
ខ្ល	(II) containing (I) plus at least part of an expressible nucleic acid(III); (c) vector containing (I), the system of (a), or (II); (d) cells,
ខ្លួ	particularly plant cells, containing (I), the system of (a), (II) or the vector of (c); (e) plants containing cells of (d); (f) seeds from the
ខ្លួ	plants of (e); (g) hybrid seed produced by crossing a male sterile plant of (e); (h) production of male sterile plants by introducing (II) into a
88	cell and regeneration to a plant; (i) restorer plants containing in one (or preferably many) cells a construct (IIa) of (I) and a sequence that
88	encodes an invertase different from the plants endogenous invertase; (j) plant that contains in one (or preferably many) cells both (II) and (IIa)
38	(k) seeds from plants of (i) and (j); (l) fruits, particularly seeds and enclared by plants of (e). (i) and (i): and (m) method for

cloning a promoter that is functionally homologous with (I). Constructs containing (I) and an invertase-encoding sequence are used to produce male-sterile plants (by co-suppression or antisense techniques) for preparation of hybrids, while constructs that contain (I) and a heterologous invertase-encoding sequence are used to prepare restorer plants (which allow propagation of the male-sterile plants). Seeds from these plants are used for in vitro embryogenesis of haploid or (double) diploid plants, and the new plants particularly produce seedless fruits. (I) can also be used to prepare transgenic plants that show increased or reduced production of endogenous materials, e.g. of plant hormones or proteins involved in provision of energy to developing tissue. (I) provide high level expression in a tissue- and time-specific manner, and do not require exogenous stimuli (e.g. temperature or chemicals) for regulation

Sequence 4135 BP; 1212 A; 774 C; 825 G; 1318 T; 0 U; 6 Other;

Gaps ; 0 Length 4135; 4; Indels Score 997; DB 4; L Pred. No. 8.6e-198; 0; Mismatches 4; Query Match
Best Local Similarity 99.6%;
Matches 997; Conservative 0 ò

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1797 ITAATGAAAGCAGAITTTGACCCATACAAAATATATGACAAAAATTGCTTCCAAAGAAAACA 1856 TGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATC TGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATC TTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAAATTGCTTCCAAAGAAACA 601 1737 661

1857 TGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGA 1916

TGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATTATAAGA

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8 Вb

1976 2036 2037 AATATAGAAGATTAGATCAATTAACAAAGGTTATGGTGGAGTGGTAAGCAGAGGCGGACC 2096 960 ATAGTGTTTTTTTTTTTTTTTTTCATATCTAAGGAGTAAAGCAACCATGAATAGAAAAGG CTTAGTAACTATATATATATAGGAATGGTGTTTTTTTTTAAATATGGATAAAATTTGTG AATATAGAAGATTAGATCAATTAACAAAGGTTATGGTGGAGTGGTAAAGCAGAGGCGGACC 2097 rargranaradaageercaccacracracaaaarccee 2137 TATGLGTTATAGTAAGGGGTCACCCACTACTAGAAATCCGG 1001 1917 1977 901 961 781 841 g ò d g ò 셤 ò

ADL17884 standard; cDNA; 158001

ADL17884;

06-MAY-2004 (first entry)

Human phosphotyrosyl phosphatase activator, PTPA, gene.

Human, ds, antisense, phosphotyrosyl phosphatase activator, PTPA, hyperproliferative disorder, developmental disorder, infection, inflammation; tumour; gene

Homo sapiens.

US2004023906-A1.

05-FEB-2004.

01-AUG-2002; 2002US-00211179

01-AUG-2002; 2002US-00211179.

(ISIS-) ISIS PHARM INC.

Dobie KW; Dean NM,

WPI; 2004-132607/13.

New antisense compound targeted to a nucleic acid molecule encoding phosphotyrosyl phosphatase activator, for modulating expression of phosphotyrosyl phosphatase activator or treating hyperproliferative disorders

Example 15; SEQ ID NO 11; 131pp; English.

The invention relates to a compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding phosphotyrosyl phosphatase activator (FTPA), that specifically hybridises with the nucleic acid molecule encoding phosphotyrosyl phosphatase activator and inhibits the expression of phosphotyrosyl phosphatase activator and inhibits the expression of phosphotyrosyl phosphatase activator i.e. ana antisense compound and a pharmaceutical carrier or diluent, a method of inhibiting the expression of phosphotyrosyl phosphatase activator in cells or tissues, a method of treating an animal having a disease or condition associated with phosphotyrosyl phosphatase activator in cells or tissues, an antisense compound. The disease or condition is a hyperproliferative disorder or developmental disorder. The compound, particularly the disorder or developmental disorder. The compound, particularly the antisense oligonucleotide is useful in modulating the function of nucleic antisense compound can also be used as research tools and diagnostics. It can also be used as tools in differential and/or combinatorial analyses to elucidate expression patterns of a portion or the entire complement of genes expressed within cells and tissues. The compound can also be used for treating diseases or conditions associated with phosphotyrosyl

(first entry)

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Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                               Haematopoietic cell proliferation disorder related DNA sequence #386.
                                                                  Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                            Piepenbrock C, Adorjan
Lipscher E, Maier S,
                                                                                                                                                                                          26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                 26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                                                                                                        Lipscher E, N
Ziebarth H;
                                                                                                                                                                                                                                         (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                          WPI; 2003-018942/01.
                                                                                                                                             WO200277272-A2
                                                                                                                      Homo sapiens
                         16-JAN-2003
                                                                                                                                                                    03-OCT-2002.
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Schwope I,
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phosphatase activator, preferably hyperproliferative disorder or developmental disorder. The compound can also be used as prophylaxis, e.g. to prevent or delay infection, inflammation or tumour formation. present sequence is the human PTPA gene which is a target for the antisense oligonucleotides of the invention.
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                                                                                        Score 55.6; DB 12; Length 158001;
Pred. No. 0.085;
1; Mismatches 460; Indels 5; G
                                                                      Sequence 158001 BP; 34764 A; 40497 C; 41696 G; 40433 T; 0 U;
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nes 460; Indels
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Pelet C,

Guetig D, Howe A, Mueller J; P, Grabs G, Lesche R, Leu E; Model F, Mueller V, Otto T,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocytic leukaemia and actor, repellent leukaemia; as probes for determining the cytosine methylation state and/or single nuclectide polymorphisms (SNPs) of haematopietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic call proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
                                                                                                                          differentiating between hamatopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CDG dinucleotides within the target nucleic acid. ABZ030861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between hally hamatopoietic cells and proliferative disorder haematopoietic cells in acute acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2550 TTTTAATTTAATTTAAATTTAATTTTATTTTTATTTTCATTAATATTTAATTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
                                                                                        present invention describes a method for detecting
Claim 28; SEQ ID NO 386; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tich 5.5%; al Similarity 42.8%; 395; Conservative
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123 GATTAAATGTGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGAATATCAAGCA 182

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ABZ10246/c ID ABZ10246 standard; DNA; 8056 XX

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The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated genes (II) having sequences (ABQ66971-ABQ67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation.
                                                                                                                                                                                                                                                                                                                                            psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Croin's disease. Note: The sequence dated for this patent did not form part of the printed specification, but was obtained in electronic formadirectly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                           nucleic acid fragments from chemically treated angiogenesis-
ociated genes, useful for determining methylation status, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37515 BP; 11428 A; 425 C; 7165 G; 18497 T; 0 U; 0 Other;
                                                                                                                                                                                                                          Claim 1; SEQ ID NO 28; 41pp + Sequence Listing; German.
                                                                                                                                                                                       associated genes, useful for dete
diagnosis or treatment of cancer.
                                                         06-DEC-2001; 2001WO-EP014320
                                                                                06-DEC-2000; 2000DE-01061338
                                                                                                                                                    WPI; 2002-500450/53.
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                                                                                                                                                      GTAGTGATTGTCTTTTATCTAGAGAGAAGTCTGCTTTTCAAAGAATATTTTTATCAGAG
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                                                           AGGTGGATGATTCTTCTTTTTGACAATGATGATGATGATGATGATGATGATGATGGTGGGA
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                                                                       AAAGTCTGCTTTTCAAAGAATATTTTATCAGAGAATATTACATCCCCCTCTCTCCCTAT
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                                      4.
Length 37515;
                                    Indels
5.5%; Score 54.8; DB 6;
llarity 46.4%; Pred. No. 0.1;
Conservative 1; Mismatches 278;
                 Similarity
                                      Matches 245;
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869 GTTTTTTCTTTAAATATGGATAAAATTTGTGAATATAGAAGATTAGA 916

Human; anglogenesis; methylation; eye disease; glaucoma; tumour; inflammation; rheumatoid arthritis; diabetic retinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiarteriosclerotic; ds.

Homo sapiens

Human angiogenesis associated polynucleotide SEQ ID NO 28.

(first entry)

28-AUG-2002

ABQ66998;

BP

ABQ66998 standard; DNA; 37515

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633 ITTCTACGATACTGCTTCATGTCAATCTTAATGAAAGCAGATTTTGACCCATACAATAA
                                                    693 TATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATATCGTTAGACTGTT
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30-JUN-2000; 2000DE-01032559.
01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metastasis associated gene; cytosine methylation; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, ADDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAATAAAATATTTTTTTGAATATTCTATTATAAAAACTAGCTGTTAGCACTCGACCTCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 113515 BP; 35172 A; 1174 C; 22520 G; 54649 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiathritic; antidiabetic;, antipsoriatic; antianiflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                           cytosine methylation; antiasthmatic;
5.4%; Score 54.4; DB 6; Length 113515; 46.1%; Pred. No. 0.14;
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                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 2148.
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                                                                                                                                          ABL34175 standard; DNA; 113515
                                                                                                                                                                                                                                                                                                                           immune system disease;
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01-SEP-2000; 2000DE-01043826.
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nes 178; Conservative
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                                                                                                                                                                                       ABL34175;
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3747 AAAATATACCTATTTTTATAATAATATTTTATTTTATAAAATATTTAACAATTCCAC 3688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human metastasis associated genes which are modified by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention
                                                           ATAATATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATATCGTTAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; gene therapy; cancer;
ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human metastasis associated gene SEQ ID NO:
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The invention relates to a nucleic acid comprising a sequence of at least with cell signalling. The activity of the modified sequences of the modified sequences of the invention may be described as cytostatic. The object of the invention is to provide the chemically modified DNA of genes associated with cell signalling, as well as object of the invention is to provide the chemically modified DNA of genes associated with cell signalling. Sa well as object of the diagnosis and/or therapy of genetic and epigenetic parameters of genes associated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis and therapy of diseases such as solid tumours and cancer. The sequences given in records ABL/0111-ABL/0626 represent chemically pre-treated cancer the sequence data for this parent is not represented in the printed sequence data for this parent is not represented in the printed sequence information supplied by the
Cell signalling, cytosine methylation; cell signalling disease; cancer;
tumour; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signaling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signaling.
                                                                           4954 TGGGATTGTAAGTTATATAGTATATTGTTTGTAAGTTATTTTTAATTTTAAGGAGTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemically treated cell signalling DNA sequence complementary to#215.
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                                                                                                                                                                                                               869 GITTITITIAAATAIGGATAAAATITGI
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01-SEP-2000; 2000DE-01043826.
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DB 6; Length 8201; 99; Indels

5.3%; Score 52.6; DB 53.1%; Pred. No. 0.23; tive 0; Mismatches

Query Match 5.3 Best Local Similarity 53.1 Matches 112; Conservative

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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regularory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG mincleotides within the target nucleic acid. ABZ03861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute of ymphocytic leukamia and acute myelogenous leukamia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related becaused for detecting a predisposition to, differentiation can also be used for detecting a predisposition to, differentiation between sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between sequences in an action of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative
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                                                          4894 iGitaradaratugagdahGirititahGrugaratititititicgraatitaatrahGr
                                                                                                                                            Human, haematopoietic cell proliferation disorder, cytostatic, gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia;
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P, Grabs G, Lesche R, Leu E;
Model F, Mueller V, Otto T, F
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Lipscher E, Maier S,
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disorders allowing for improved and informed treatment of patients
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                Seguence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                     Human, immune system disease, cytosine methylation, antiasthmatic; antiatretisoclarotic; antianaemic; cytostatic, nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhetmatic; antiarthritic; antidabetic; antipsoriatic; antilaflammatory; cancer; eye disease; arteriosclerosis; anaemia; antilinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Albrimar's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid comprising fragment of chemically modified gene, useful f
diagnosis and treatment of diseases associated with abnormal cytosine
methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13020 GATATATAAAAAGGTTACGTGGTATTAGAGAAAAGATGGATTATTAATAAAIGGTGTT
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Pred. No. (
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                           DNA; 13584
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01-SEP-2000; 2000DE-01043826.
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al Similarity 46.6%;
264; Conservative
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Best Local Similarity
                        ABL32615 standard;
                                                                                                                                                                                                 Human immune
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                                                                               ABL32615;
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                                                                                                                                                                                                                                                                                                                                   475
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G, Lesche R, Leu E;
Mueller V, Otto T, Pelet
                                                       13140 TATATATATTTTTTTAATTGATTAAAGGTTTAAATAGAAAAGGTAAAATTTTAAATTTTT
                                                                                                                                                                                                                                                                                                                                   AGAAAGGTAGTGATTGTCTTTTATCTAGAGAAAAGTCTGCTTTTCAAAGAATATTTTTA
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P, Grabs
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Lipscher E, Maier S,
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, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG.
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Schwope I,
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for

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1658
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differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells, for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single mucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferation of haematopoietic cell proliferation of haematopoietic cell proliferation disorders. The present method enables highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGATCTGAATTTATAAGAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                          GATICITCITITIGACAATGATGAATGA-----TGGGCAAATACTAGAATGTTGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATGAGGTGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 CCTTCTCGGATCTAATGAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGG
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                                                                                                                                                                                                                               Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
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Pred. No. 0.55;
2; Mismatches 494;
                                                                                                                                                                                                                                                            Best Local Similarity 44.1%;
Matches 410; Conservative 2
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Human, tumour suppressor gene, oncogene, antitumour, cytostatic, cancer, tumour, CpG dinucleotide, single-nucleotide polymorphism; SNP; cytosine methylation; ds.
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                                                                                                  TITITICITITICITITICATATCTAAGGAGTAAAGCAACCATGAATAGAAAAGGCTTAGTAA
                                                                                                                                                                                                                                                                                                                                                                                          CTATATATCAAAGGAATGGTGTTTTTTTTTAAATATGGATAAAAATTTGTGAATATAGA
                AAAAGTACATACACCAAGAATATTCAATAAAATATTTTTTGAATATATTTTAAAAA
                                                                                                                                 CTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCATTT
                                                                                                                                                                                        ACTAATCGACCTCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATCTTAATGAA
                                                                                                                                                                                                                                                AGCAGATTTTGACCCCATACAATAATATGACAAAATTGCTTCCAAAGAAAACATGGCTCTT
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07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes a novel reagent for diagnosis, molecular definition and therapy of chronic inflammatory joint disease, and other inflammatory diseases; and other products of the invention have antiinflammatory, cytostatic, antisheumatic and immunosuppressive activity and can be used for gene therapy. The reagent of the invention and any proteins and antibodies derived from it, are used (i) for analysing tissue and blood samples for medical diagnosis; (ii) for diagnosis and characterisation of chronic joint diseases, on the basis of molecular characterisation of determining the etiological pathogenicity principle of as yet uncharacterised inflammatory diseases, also monitoring progression and/or treatment of disease, and optimisation of therapy and (iii) for developing treatments for inflammatory diseases, particularly of joints, infections and tumours, ACA64801-ACA64965 represent human polymucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      369 ATTGECTTTATCTAGAGAGAAGTCTGCTTTTCAAAGAATATTTTTATCAGAGAATATT 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reagents for diagnosis, study and therapy of chronic inflammatory joint and other diseases, comprises any of many specified genes or derived
                                             844 AGTAACTATATATCAAAGGAATGGTGTTTTTTTCTTTAAATATGGATAAAAATTTGTGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 115218 BP; 35618 A; 23477 C; 22286 G; 33837 T; 0 U; 0 Other;
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antiinflammatory, cytostatic, antiarthritic, antirheumatic,
immunosuppressive, gene therapy, etiological pathogenicity; ds
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                                                                                                                                                                                                                                                                                         Human HNRNP GP43 DNA corresponding to AL034397.
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                                                                                                                                                                                                                                                              (first entry)
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polyglutamine disorder; solid tumour.

WO200192565-A2

Unidentified.

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with beaving a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single complexide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing diseases or the predisposition to specific diseases, by analysing cortisions. The parameters may be compared to another set of gentic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences detain electronic format directly from WIPO at
genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5413 BP; 1391 A; 65 C; 1102 G; 2855 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                       Claim 1; SEQ ID NO 417; 27pp; English
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1323 ATATATATATATATATATATATATATATATATA-TTTTATATATATATATATATATATATATA 1381 1382 TATATATATAGAGGTATTTTTATTTTATTTTATAGAGGTATTTATATATATATATTTT 1441 652 TGTCAAATCTTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAATTGCTTCCA 711 771 772 TITATAAGAATAGTGTTTTTTTTTTTTTTTTTTTTAAGGAGTAAAGCAACCATGAA 831 712 AAGAAAACAIGGCICTIAIAGIGAAAIAICGIIAGACIGIIAIAGAAAGAICIGAAITIA Gaps .. H 5.0%; Score 50; DB 4; Length 5413; ilarity 51.5%; Pred. No. 0.77; Conservative 0; Mismatches 130; Indels 1502 ATTTTTTATATATAGGTATTTATATTTAT 1531 892 AAATTTGTGAATATAGAAGATTAGATCAAT 921 Similarity 139; Query Match Local Matches g g PP δ g à ò ઠે

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DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA, cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropotesis; neurodegenerative disorder; wardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndrome; myelodysplastic syndr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA transcription associated complementary genomic DNA #103.
                                                                                                                              ABK28332 standard; DNA; 11745
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (DNA) coligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the transcription state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription

(particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, haematological disorders, immunological disorders, where syndrome, neurological disorders, neurodegenerative disorders, waardenburg currone, immuno-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, syndrome, Niemann-Pick disease, myslodysplasic, some second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  192 GATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATGAGGTGGATG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumors or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infarction, hypertension, angiogenesis, erythropojesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from the European Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 TGATTAAATTAATTAATATGTATGACAAAGGATTAAACCTAGTTAATGATAATAACTTC
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                                                                                                                                                                                                                                                                                     06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-UJW-2000; 2000DE-0103529.
01-SBP-2000; 2000DE-01043828.
                                                                                                                                                                                                                              06-APR-2001; 2001WO-EP003973.
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Direct Submission

Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr -
Web : www.genoscope.cns.fr -
Obetermination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Gosoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Gosoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Sucer Genetics at the Roswell Park Cancer Gosoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Bosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.cdu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Submitted (02-UUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr.
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/clone="BACR29B23"
/clone=ib="RPCI-98"
/note="end : T7"
                                                                                                                                                                                                                                                 91; Mismatches 227;
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr
- Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffallo, NY. The library is named RPCI-99 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library.
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit
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Neoptera; Endopterygota; Diptera; Erachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
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      209;
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Principle Deviation of this BAC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gosegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be licentially a thitp://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : seqref@genoscope.cns.fr
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       BACROSK10 of RPCI-98 library from Drosophila melanogaster (fruit
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Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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15.8%; Pred. No. (
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                            fly), genomic survey sequence.
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melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the pisogenic strain y2; on bw 8p, the same strain used for the BDGP's pland BAC and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers
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al Similarity 31.1%; Pred. No. 0.011;
201; Conservative 114; Mismatches 330;
                                                                                                                                                                                                                                                                                                                     /mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR29B23"
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/note="end : T7"
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CACCAAGAATATTCAATAAAATATTTTTTTGAATATTCTATTATAAAAACTAGCTGTTAG

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GSS 03-JUN-1999 end of BAC #

CNS0039G 1101 bp DNA linear Drosophila melanogaster genome survey sequence TET3

LOCUS RESULT 4 CNS0039G

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Best_Local Similarity 37.5
Matches 209; Conservative
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Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                    CNS020K7 1092 bp DNA linear GSS 01-SEP-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 222L11 of library G from Tetraodon nigroviridis, genomic survey
                                                                                               619
                                                                                                                                                  ACCCATACAATAATATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATA 739
                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi; Atinopterygii, Neopterygii, Taleostei, Buteleostei, Neoteleostei, Acanthomoxpha; Acanthopterygii, Percomoxpha; Tetraodontiformes; Tetradontoidea, Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
CACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCATTTACTAATCGACC
                                                                          TCGATTACATCACTTTCTACGATACTGCTTCATGTCAAATCTTAATGAAAGCAGATTTTG
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6.0%; Score 60.2; DB 9; Length 1
Best Local Similarity 38.7%; Pred. No. 0.046;
Matches 104; Conservative 45; Mismatches 120; Indels
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|mol_type="genomic DNA"
|db_xref="taxon:99883"
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Tetraodon nigroviridis
Tetraodon nigroviridis
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/clone_lib="G"
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; on bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be location/Qualifiers
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BAC: POST SPORTS OF RPCI-98 library from Drosophila melanogaster (fruit
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                                      774 WAAAWWUTWITIAWITITAWWATWAWWITWITITTTAAAWAAAANAWTITTAWIAAA
                                                                                                                                                                                                                                                                  TAAGAATAGTGTTTTTTTTTTTTTTTTTTAAGGAGTAAAGCAACCATGAATAGA
   AAATCTTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAATTGCTTCCAAAGA
                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster
Eukaryota, Merazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
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/mol type="genomic DNA"
/db_xref="taxon:7227"
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/clone_lib="RPCI-98"
/note="end : TET3"
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186 AATAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATGAGG 245
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                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                         /sex="male"
/tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                       DB 9; Length 1542;
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0; Mismatches 525; Indels
                                                                           1. .1542
/organism="Mus musculus molossinus"
/moltype="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-201G10.TJ"
                                                                                                                                                                                                                                                                                           Score 59;
Pred. No.
                                                         Location/Qualifiers
pBACe3.6
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Best Local Similarity 43.8%;
Matches 420; Conservative
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail)-hattoringsor.riken.go, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp
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Mus musculus molossinus DNA, clone:MSMg01-201G10.TJ, genomic survey
                                                                                                                                                                                                                            160 TNANTATANTANATANANANTNANATATATAANANTNTNTATATAGWGANWNWNATA 219
                                                                                                                                                                                                                                                                                                           302 ACCCTTCTCGGATCTAATGAAAAGTAT-GGAATAGTAGATAATCGAATCTCTTTAGAA 360
                                                                                                                                                                                                                                                                                                                                                                                     340 TAAATTAATTAWITWAAAAAAAATTWIATTTATATATAAAAATTTATTATATAAAA 399
                                                                                                                                                                                                                                                                                                                                                                                                                             361 AGGTAGTGATTGTCTTTTATCTAGAGAGAAGTCTGCTTTTTCAAAGAATATTTTTATCAG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCAATCCTAAAAGTACATACACCAAGAATATTTCAATAAAATATTTTTTTGAATATATTTT 540
                                                                             122 AGATTAAATGTGATGTYCATTCCAATATTTCAAGATCATTAATGATAGGGGAATATCAAGC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    99
                                                                                                                                                                                             AATAAATAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAAT
                                                                                                                                                                                                                                                                      242 GAGGIGGATGATICTITITIGACAAIGAIGAAGAAGGAGCAAATACTAGAATGTIGGG
    ATATATATTTANATATNITATANANTATAAANTNITANANTNWNTATATAAAAANTCTN
                                        62 ATAATAACTICAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chouv. Tsurumi-ku, Yokohama, Ranagawa 230-0045, Japan [E-mail:hattoriogsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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                                                                                                                                                                                                   385 AGAGAAAGICTGCTTTTCAAAGAATATTTTATCAGAGAATATTACATCCCCCTCTCTCC 444
265 ACAATGATGAATGATGGGCAAATACTAGAATGTTGGGACCCTTCTCGGATCTAATGAAAA 324
                                                                                                                                                                       AAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGGTAGTGATTGTCTTTTATCTAG 384
                                                                                                                                                                                                                                                                                                                   825 WAAAHWATTAAAAAAAAAAAAAAAAAAWWTAWWTAWTWAAATYWAAYTTAAAWTTWAWAA 884
                                                                                                                                                                                                                                                                                                                                                                885 AAATWWWTTTTTTTTTTTTTYYCCSSSCSSSSSSSSSCCVAAAATTAWWAATKT 944
                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mu
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505 AGAATATTCAATAAAATATTTTTTTGAATATTCTATTATAAAACTAGCTGT
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus molossinus"
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/sub_species="molossinus"
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/clone="MSMg01-093J24.TJ"
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AG311015.1 GI:47883969
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Mus musculus molossinus
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Direct Submission

Direct Submission

BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkely Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruttly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain to for Drosophila DNA provided by the BDGP from the isogenic strain y2; no bw sp, the same strain used for the BDGP's pl and bw to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR31021 of RPCI-98 library from Drosophila melanogaster (fruit AL071063
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          184 ATTITITABATATIAANTAAATINTATAAANNNNGTGGGGGGGGCCNCACACACACACACAC 125
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                                                       900 GAATATAGAAGATTAGATTAACAAAGGTTATGGTGGAGTGGTAAGCAGAGGGGGGAC
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster
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/db_xref="taxon:7227"
/clone="BACR31021"
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/note="end : TET3"
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3ACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit

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                                                                                                                                                                                 188 TAACGATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATGAGGTG 247
                                                                                                                                                                                                                                                            GATGATTCTTCTTTTTGACAATGATGATGATGGCCAAATACTAGAATGTTGGGACCCTT 307
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                                                                            594 TTAGATAAAAAATAATAATAATNAAAAGATAATTAAATATAATAATAAAAATATAAAATA
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                                                   8 ACTITIGATITAAATITAATITAATATIGACAAAGGATITAAACCTAGTIAATGATAATA
 Length 2015;
                         532; Indels
  DB 9;
 Score 58.8; DB 9
Pred. No. 0.086;
1; Mismatches 53
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CNSOODKY 928 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC #

LOCUS

RESULT 10 CNS00DKY

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Submitted (02-UWN-1999) Genoscope - Centre National de Sequencage :

No Submitted (02-UWN-1999) Genoscope - Centre National de Sequencage :

No Submitted (02-UWN-1999) Genoscope - Centre National i sequef@genoscope.cns.fr

No Benoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BBCP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoscaper in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecotic digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                    Pterygota;
                                                                                                                                  Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygo
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
(Pases 1 to 928)
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32.1%; Pred. No. 0.097;
ive 67; Mismatches 258;
                                                                                       Drosophila melanogaster (fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila m
/mol_type="genomic DNA"
/db_xref="taxon:7227"
fly), genomic survey sequence.
AL071865
AL071865.1 GI:4948170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="BACR27A24"
/clone_lib="RPCI-98"
/note="end : T7"
                                                                                                                 Drosophila melanogaster
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Matches 157; Conservative
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                       ACCESSION
VERSION
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Swarterosters aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Acuthomoterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomotepha; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.

E 1 (bases it of 1335)

Expressed sequence tags from Gasterosteus aculeatus
Unpublished (2004)

Contact: Gimwood, Jane
Stanford Human Genome Center
Stanford University School.of Medicine
Stanford University School.of Medicine
975 S California Avenue, Palo Alto, CA 94304, USA
Tel: 650 320 5917

Fax: 650 320 5801

Email: jane@ehgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Blood"
/clone_lib="CR1213"
/clone_lib="CR1213"
/note="Vector: pTARBAC2.1; Site_1: ECORI; The sequence of the clone was established as a mapping and sequencing collaboration at the Stanford Genome Evolution Center, funded by the NIH Centers of Excellence in Genomic Science (CEGS) initiative (http://cegs.stanford.edu). The clone was isolated from the BAC library CHORI-213 built by pleter decong in collaboration with the Stanford Genome Evolution Center (http://www.chori.org/bacpac/). Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CL646802 1335 bp DNA linear GSS 06-JUL-2004 CH213-123P18.SP6 CH213 Gasterosteus aculeatus genomic clone CH213-123P18 3', genomic survey sequence.
                                                                                                                                                                                                                                                  CICAAICAAICCIAAAAGIACAIACACCAAGAAIAIICAAIAAAAIAIITITIGAAIAI 535
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                                                                                                                      361 AGGTAGTGATTGTCTTTTATCTAGAGAGAAAGTCTGCTTTTCAAA-----GAATATTTTT
                                      301 GACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAGATAATCGAATCTTTAGAA
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GSS.
Gasterosteus aculeatus (three spined stickleback)
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/strain="Salmon River"
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High quality sequence stop: 686.
Location/Qualifiers
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/clone="CH213-123P18"
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Class: BAC ends
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CL646802/c
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                          Sorghum propinguum
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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TGGTGTTTTTTCTTTAAATATGGATAAAATTTTGTGAATATAGAAGATTAGATTAA
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Corganism="Sorghum propinguum"

/mol type="genomic DNA"

/db xref="texon:132711"

/clone="SP Ba0057N22"

/clone 11bb="SP Band"

/note="Wetcor: pBeloBACI1; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
8521-0088, USA
171: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 132)
Wing, R., Yu, Y., Kim, H.R., Collura, K., Pries, G., Currie, J., Soderlund, C. and Hatfield, J.
Sequencing of Sorghum BAC ends.
http://genome.arizona.edu/stc/sorghum
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                                                                                                                                                                                                                                BZ695089 1132 bp DNA linear GSS SP Ba0057N22.f SP Ba Sorghum propinguum genomic clone SP Ba0057N22 5', genomic survey sequence.
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45.5%; Pred. No. 0.11;
iive 1; Mismatches 290;
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BACKWARD: gta aaa cga cgg cca gtg
plate: 0057 row: N column: 22
Seg primer: atc agc ggc cgc gat cc
Class: BAC ends.
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PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                               BZ695089
BZ695089.1 GI:28387830
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                                                                                                                                                           Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Detexiniation of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Uong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                               195 AAATGGCATTAAAGTAAATAAGGAGAAATGATTCACCCAATATTGAATGA-GGTGGATGAT 253
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http://www.chori.org/bacpac/ordering_information.htm)
                                                                                                                                                                                                                                                                   254 TCTTCTTTTTGACAATGATGAATGATGGCCAAATACTAGAATGTTGGGACCCTTCTCGGA
                                                                                       Gaps
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                     Length 1335;
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                                                 Score 58.4; DB 9; Pred. No. 0.11; I; Mismatches 319;
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BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain vse for the BDGP isogenic strain vse for the BDGP PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          538 TATTATAAAAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAG
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Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                       58; Mismatches 312; Indels
                                                                                                                                                                                   /organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACROBKO8"
/clone_lib="RPCI-98"
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fly), genomic survey sequence.
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                                                                                                Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565
                                                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (S-mail : segref@genoscope.cns.fr
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BACN15KO5 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Drosophila melanogaster"
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Drosophila melanogaster
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/db_xref="taxon:7227"
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/clone=lib=DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/mol_type="genomic DNA"
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٠	PRIOR FIL	SEO DA	Ž N	1999-08 S: 23	20-24						
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엄	Ñ	σ	RMYC	: ::: KYRRWYN	:: INKSR	::: WWKGWYKP	: : : : : : : : : : : : : : : : : : : :	:: ::::: BRYHARRWKDMKTAYBMTMTNKW	: : :DMKTAYBM	.: TMTNKW	1118
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g	11	9 GKT	::: WRHR	:::: : YWRWRAM	:::	::::: DHHYVTAN		DKDDKRTRW	: : H WWKKNNNA	TGWDD:	178
ò	13	v	ATTC	AATAŢTŢ	CAAG	ATCATTA?	GTYCATTCAATATTCAAGATCATTAATGATAGGGGAATATCAAGCAATAAA	ATATCAAGO	AATAAATA	TAAÇGATA	195
q	17	σ	:: MWNN	 NGCBTVT	WMVR	XKTDRDWS	::::::::::::::::::::::::::::::::::::::	* : : : : : WINNWSYDVT	IGGWAMMXX.	HOKRKY	7 238
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ò	25.	н	CTICI	TTTTGA	CAAT	GATGAATC	TTTGACAATGAATGAATGGGCAAATACTAGAATGTTGGGACCCTTCTC	ACTAGAATG	TTGGGACC	CTTCTC	310
d	29	σ	NSTC	TWKSKT	TKVF	TSCWANNO	: :	* * * * † WWKWSAAMG	: VYWNNNNN)	: : NNWTYR	358
ò	31	11 GGAT	CTAA	TGAAAAA	AGTA	TGGAATAC	GGATCTAATGAAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGGTAGTGAT	AATCTCTTŢ	AGAAAGGT	AGTGA	370
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TRAMITMRWIMKGDGMIVRKKVKWRDIICIYVDVWADSWVWWYANWMRCRDVIYIRNNIYC 574
                                                                                                                                                                                                                                                                                                          AAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGACTACTCGGTTACGAGCCCTGTCA 605
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                                                                 KSYAHSYWYWSNNAMWYRRYSARNWSSMARWITRNNWWMSGBVRMRWAGTMWWRHWNNNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REPERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
FRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
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5.0%; Score 50.4; DB 4; Length 1055;
Best Local Similarity 20.6%; Pred. No. 0.0045;
Matches 181; Conservative 188; Mismatches 504; Indels 5
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OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. FAE1 promoters
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                                  TGTCTTTTATCTAGAGAGAGAAGTCTGCTTTTTCAAAGAATATTTTTATCAGAGAATATTAC
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TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin version 3.0
LENGTH: 1141
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ORGANISM: Artificial sequence
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US-09-806-708B-22/c
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-66
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4.9%; Score 48.8; DB 4; Lengtn 8
Best Local Similarity 10.8%; Pred. No. 0.01;
Matches 29; Conservative 136; Mismatches 103; Indels
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APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GRNSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 2813

LENGTH: 832
                                                                                                                                                                                                                                                                            Score 49.2; DB 4; I Pred. No. 0.014; 0; Mismatches 98;
## PRIOR FILING DATE: 2000-04-07
| PRIOR APPLICATION NUMBER: DE 10032529.7
| PRIOR PILING DATE: 2000-06-30
| PRIOR FILING DATE: 2000-09-01
| PRIOR FILING DATE: 2000-09-01
| NUMBER OF SEQ ID NOS: 98
| LENGTH: 5360
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                4.9%;
52.4%;
                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 52.4
Matches 108; Conservative
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US-09-621-976-2813
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                                           253 TICTICTITITGACAATGATGAATGATGGGCAAATACTAGAATGTTGGGACCCTICTCGG 312
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APPLICANT: OLEK, Alexander
APPLICANT: PIEPRBRROCK, Christian
APPLICANT: PIEPRBRROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
TITLE OF INVENTION: DA Sessing DNA Methylation
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/204,708
CURRENT APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2001-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR FILING DATE: DO00-04-06
PRIOR FILING DATE: D000-04-06
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Patent No. 6677731
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     644 CTGCTTCATGTCAAATCTTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAAT 703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 YYASTNCTWSTCRWKTARGWWYYAMRYYTWAKASGCNNNAKWRCAWWYACATNNNAMAWW 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    524 ITTTTTGAATATTCTATTATAAAACTAGCTGTTAGCACTCGACCTCGGTCGYTATTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 584 TACTCGGTTACGAGCCCTGTCATTTACTAATCGACCTCGATTACATCACTTTCTACGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: promoter DOCATION: (1)..(1055) OTHER INFORMATION: consensus sequence of A.t. and L.a. FAE1 promoters US-03-806-708B-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                  PATENT NO. COLLING.
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REPERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US 60/147,133
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
4.7%; Score 47.2; DB 4; Length 1055;
Best Local Similarity 18.8%; Pred. No. 0.027;
Matches 90; Conservative 145; Mismatches 242; Indels 1
                                                                                                   :|::::::|:::|
KAWRASCMMRRKYAGKSKTSYKSMWMCW 268
                                                                        961 TATGTGTTATAGTAAGGGGTCACCCACT 988
                                                                                                                                                                                                        Sequence 23, Application US/09806708B Patent No. 6784342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial sequence
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US-09-806-708B-23/c
                                    181
                                                                                                               241
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RESULT 7 US-09-248-796A-729

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Sequence 729, Application US/09248796A

Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL REITH Weish Weish Weish William AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS FITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-02-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 729
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
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4.6%; Score 46; DB 4; Length 114
Best Local Similarity 50.5%; Pred. No. 0.053;
Matches 109; Conservative 1; Mismatches 106; Indels
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; Pred. No. 0.042;
. 0; Mismatches 106;
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US-09-270-767-29120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 4.6%;
Best Local Similarity 50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Candida albicans
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US-09-270-767-29120
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APPLICATION NUMBER:
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IMMEDIATE SOURCE
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GAAAAAATCTTTATGAAAACTTAAATAAAGGAAAACTGAAAAGAAAATCGAGGCATATAT 301
                                                                                                                                                                                                                            APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13204
LENGTH: 2396
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Pred. No. 0.066;
1; Mismatches 106; Indels
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Sequence 14, Application US/08232463

Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 5-
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198 TGCCATTAAAGTAAATAAGGAGAATGATTCACCCAA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 regearraacracaraaarraaarraaraaaeea 397
                                                                        362 icgcarradgeracaraaarraaarraaaareea 397
                                   TGGCATTAAAGTAAATAAGGAGAATGATTCACCCAA
                                                                                                                                                  S-09-270-767-13204
Sequence 13204, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13204
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 109; Conserva
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APPLICANT: Cohen, Daniel
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Marta
APPLICANT: Blumenfeld, Lydie
APPLICANT: Bouqueleret, Lydie
APPLICANT: Bother Berler
TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REPERENCE: GENEST: 047405
CURRENT APPLICATION NUMBER: US/09/539,333D
CURRENT FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: US 60/126,903
PRIOR APPLICATION NUMBER: US 60/131,971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      252 ATTCTTCTTTTTGACAATGATGAATGATGGGCAAATACTAGAATGTTGGGACCCTTCTCG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 CAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAGAAGATTAAATG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 GATCTAATGAAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGGTAGTGATT 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 157; Indels
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                                        EP 91 114 300.6
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US/07/935,313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 3.7%; Prec
14; Conservative 210;
                                                    ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                   REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                     TELEX: 899149
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
                                                                                                                                                                                                                      (703) 683-4109
                     FILING DATE:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: sing
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                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 14; Conserv
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/KEY:
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LOCATION: 31..1107
CTHER INFORMATION: 5'regulatory region g35018 gene
FEATURE:
NAME/KEY: exon 1289
OTHER INFORMATION: exon A g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AME/KEY: misc_feature
OCATION: 65884..67854
THER INFORMATION: 3'regulatory region g35018 gene
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-04-30
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR FILING DATE: 1999-07-27
PRIOR APPLICATION NUMBER: US 60/146,453
PRIOR FILING DATE: 1999-07-29
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-18
PRIOR FILING DATE: 1999-10-18
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PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-18
PRIOR PILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
PRIOR PILING DATE: 1999-10-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEY: exon
LOCATION: 18778..18862
OTHER INFORMATION: exon Bbis g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
OCATION: 64666..64812
OTHER INFORMATION: exon F 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: exon
LOCATION: 25593..25740
OTHER INFORMATION: exon C 935018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: exon
LOCATION: 201188..201234
OTHER INFORMATION: exon S 935030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME: 4x01

COCATION: 14877.14920

THER INFORMATION: exon B g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAME/KEY: exon
OCATION: 29388..29502
THER INFORMATION: exon D g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AME/KEY: exon
OCATION: 65505..65853
THER INFORMATION: exon G g35018 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 214676..214793
OTHER INFORMATION: exon T 935030 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: exon
JOCATION: 29967..30282
PITHER INFORMATION: exon E g35018 gene
PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEATURE:
NAME/KEY: exon
LOCATION: 94124..94964
OTHER INFORMATION: exon 935017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: exon
COCATION: 240528..240569
CTHER INFORMATION: exon M1117 complement g34872 gene
FEATURE:
                                                                                                                                                                                                                                                                                                                                            AME/KEY: exon
JOCATION: 215819..215975
JTHER INFORMATION: exon Rbis complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Index.'
REATURE:
NAME/KEY: exon
LOCATION: 237406..237428
OTHER INFORMATION: exon Nbis complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                AAME/KEY: exon
LOCATION: 216661..216952
THER INFORMATION: exon Qbis complement 934872 gene
FATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMB/KEY: exon
OCATION: 231272..231412
THER INFORMATION: exon Obis complement 934872 gene
                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 213818..215818
OTHER INFORMATION: 3'regulatory region g34872 gene
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEATURE:
NAME/KEY: exon
JOCATION: 231787...231880
THER INFORMATION: exon O2 complement g34872 gene
PEATURE:
AME/KEY: exon
JOCATION: 231879...231879...231879...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: exon
LOCATION: 239719..239807
DIHER INFORMATION: exon N2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EATURE:
AMIS/KEX: exon
OCATION: 217027..217061
THER INFORMATION: exon Q1 complement g34872 gene
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMB/KEY: exon
ACATION: 216661..217061
THER INFORMATION: exon Q complement 934872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: exon
LOCATION: 234174..234321
OTHER INFORMATION: exon O complement g34872 gene
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NAME/KEY: exon
LOCATION: 239719..239853
OTHER HFORMATION: exon N complement g34872 gene
                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 215819..215941
COCATION: 215819..215941
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AME/KEY: exon
OCATION: 229647..229742
THER INFORMATION: exon X complement g34872 gene
EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AME/KEY: exon
CCATION: 2304068..230721
THER INFORMATION: exon P complement g34872 gene
AME/KEY: exon
OCATION: 215702..215746
THER INFORMATION: exon U g35030 gene
                                                               FEATURE:
NAME/KEY: exon
LOCATION: 216836..216915
OFFER INFORMATION: exon V g35030 gene
FEATURE:
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OTHER INFORMATION: 99-27943-150 : polymorphic base G or (NAME/KEY: allele LOCATION: 21672 COTHER INFORMATION: 99-27935-193 : polymorphic base G or (NAME/KEY: allele LOCATION: 65485
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LOCATION: 95396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: 199122.201122
OTHER INFORMATION: 5'regulatory region
PRIOR PAPLICATION NUMBER: 09/539,333
PRIOR PILING DATE: 2000-03-03
PRIOR PILING DATE: 2000-03-03
PRIOR PLING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: 09/416,384
PRIOR PAPLICATION NUMBER: 09/168,088
PRIOR APPLICATION NUMBER: 60/168,088
PRIOR PILING DATE: 1999-11-30
NUMBER OF SEQ ID NOS: 134
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AME/KEY: misc feature
OCATION: 247803..249803
OTHER INFORMATION: 3'regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DUCATION: 240440..241153
OTHER INFORMATION: exon W2
NAME/KEY: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: exon
LOCATION: 201123..201560
OTHER INFORMATION: exon S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AME/KEY: exon
LOCATION: 238715..238919
OTHER INFORMATION: exon V3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 216836.,217077
OTHER INFORMATION: exon V2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOCATION: 227655..227736
THER INFORMATION: exon V4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 201123..201234
OTHER INFORMATION: exon S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION: exon V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: exon X
NAME/KEY: exon
LOCATION: 244353..244561
OTHER INFORMATION: exon Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 215702.,215746
OTHER INFORMATION: exon U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OCATION: 240440..240673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: exon T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: exon V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION: exon Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215702..215746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IAME/KEY: exon
OCATION: 246273..247802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214676..214793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241072..241291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216836..216994
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 319608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-09-679-409-1
is Sequence 1, Application US/09679409
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jetent No. 6555316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104809 ACATAATTTTTAATTTTAGAAAATTATGACAAAAACTCGTTCATTCCTTTTTTGGAAAAA 104868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104869 CGATACTTAACCCACTAGTAAATGTTAAGTCCTGCATTATGCACAGGGGTTAATAAAATTT 104928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 TGAATGAGGTGGATGATTCTTCTTTTTGACAATGATGATGATGATGGCGAAATACTAGAATG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AGAGAAGATTAAATGTGATGTYCATTCAATATTTCAAGATCATTAATGATAGGGGAATAT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 CAAGCAATAAATAAAGTGGCATTAAAGTAAATAAGAGAGAATGATTCACCCAATAT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 319608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.5%; Score 44.6; DB 4; Length 3 Best Local Similarity 49.8%; Pred. No. 0.6; Matches 113; Conservative 0; Mismatches 114; Indels
                                              LOCATION: 240528, 240596
OTHER INFORMATION: exon M1090 complement g34872 gene
                                                                                                                                                   NAME/KEY: exon
LOCATION: 240528.240617
OTHER INFORMATION: exon M1069 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: exon
LOCATION: 240528..240824
OTHER INFORMATION: exon M862 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 240528..240994
OTHER INFORMATION: exon M692 complement g34872 gene
                                                                                                                                                                                                                                                                                                   NAME/KEY: exon
LOCATION: 240528..240644
OTHER INFORMATION: exon MS2 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon.
LOCATION: 240800..240993
OTHER INFORMATION: exon MS1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: 241686..243685
JTHER INFORMATION: 5'regulatory region g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: 290652..292652
OTHER INFORMATION: 3'regulatory region g34665 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: exon
LOCATION: 240528..241685
OTHER INFORMATION: exon M1 complement g34872 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 292653..292841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        임
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LOCATION: 210361
OTHER INFORMATION: 8-283-278
NAME/KEY: allele
LOCATION: 210463
OTHER INFORMATION: 8-283-176
NAME/KEY: allele
LOCATION: 210486
                                                                                                                                                            LOCATION: 210486

OCHER INPORMATION: 8-283-153:
NAME/KEY: allele
LOCATION: 210583

OCHER INPORMATION: 8-283-56:
NAME/KEY: allele
LOCATION: 210879

OCHER INPORMATION: 8-282-345:
NAME/KEY: allele
LOCATION: 210979

OCHER INPORMATION: 8-282-260:
NAME/KEY: allele
LOCATION: 210979

OCHER INPORMATION: 8-282-245:
NAME/KEY: allele
LOCATION: 211030

OCHER INPORMATION: 8-282-245:
NAME/KEY: allele
LOCATION: 211132

OCHER INPORMATION: 8-281-367:
NAME/KEY: allele
LOCATION: 211136

LOCATION: 211136

LOCATION: 211316

LOCATION: 211316

LOCATION: 211316

LOCATION: 211316

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OCHER INFORMATION: 8-291-248:
NAME/KEY: allele
LOCATION: 212821
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OTHER INFORMATION: 8-278-289
NAME/KEY: allele
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Best Local Similarity 49.8%;
Matches 113; Conservative
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UCCATION: 20378
UCCATION: 20378
UCCATION: 20378
UCCATION: 203378
UCCATION: 204138
UCCATION: 204138
UCTHER INPORMATION: 8-296-213 : polymorphic base A or T
UCCATION: 204034
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UCTHER INPORMATION: 8-252-190 : polymorphic base A or G
UCCATION: 204034
UCTHER INPORMATION: 8-252-190 : polymorphic base A or G
UTHER INPORMATION: 8-252-190 : polymorphic base A or G
UTHER INPORMATION: 8-252-190 : polymorphic base A or G
UTHER INPORMATION: 204034
UCTHER INPORMATION: 8-252-190 : polymorphic base A or G
UTHER INPORMATION: 204034
UCTHER INPORMATION: 8-252-190 : polymorphic base A or G
UTHER INPORMATION: 204034
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LOCATION: 209631
OTHER INFORMATION: 8-285-319 : polymorphic base A or G
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       UNAME/KEY: allele
LOCATION: 107281
COTHER INFORMATION: 99-24656-260 : po
NAME/KEY: allele
LOCATION: 160640
CTHER INFORMATION: 99-24639-163 : p
NAME/KEY: allele
LOCATION: 160876
CTHER INFORMATION: 99-24634-108 :
NAME/KEY: allele
'ACATION: 168974
  INFORMATION: 99-31960-363
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LOCATION: 205206
OTHER INFORMATION: 8-295-248 :
NAME/KEY: allele
LOCATION: 205329
OTHER INFORMATION: 8-295-125 :
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LOCATION: 206545
OTHER INFORMATION: 8-292-198 :
NAME/KEY: allele
LOCATION: 207313
OTHER INFORMATION: 8-251-322 :
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OCATION: 206064
OTHER INFORMATION: 8-293-130
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TION: 208960
RINFORMATION: 8-287-249
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LOCATION: 208285
NTHER INFORMATION: 8-289-322
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LOCATION: 209123
NTHER INFORMATION: 8-287-86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09410464
Patent No. 6395892
GENERAL INFORMATION:
APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in TITLE OF INVENTION: poplar and other plant species.
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                                                             : polymorphic base A
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT PAPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SCPTWARE: Patentin Ver. 2.0
SEQ ID NO 29271
LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                              1378 ATCAAAGGATAATTCAAAATTGCATCCAAATAACAACATTAGTAATGGAAGGACTTATGG
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                                                                                                                                                                                                                                                                                                        Length 4285;
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Pred. No. 0.15;
1; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                      Score 43.8; DB 3; Length 4
Pred. No. 0.26;
0; Mismatches 112; Indels
                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Populus balsamifera subsp. trichocarpa
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: US/09/410,464
CURRENT FILING DATE: 1999-10-01
BARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
BARLIER PILING DATE: 1999-04-06
BARLIER PILING DATE: 1998-04-06
BARLIER FILING DATE: 1998-04-06
SOFTWARE: PATENTING VOICE: 2.0
SOFTWARE: PATENTIN VOICE: 2.0
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; Sequence 29271, Application US/09270767
; Patent No. 6703491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.48;
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Best Local Similarity 51.9
Matches 122; Conservative
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                                                                                                                                                                                                           LENGTH: 4285
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Best Local S:
Matches 103
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                                  Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION:
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13327
LENGTH: 2031
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Pred. No. 0.24;
1; Mismatches 100; Indels
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                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Drosophila melanogaster US-09-270-767-13327
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 50.5%;
Matches 103; Conservative
RESULT 15
US-09-270-767-13327/c
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Fri Nov 12 18:15:03 2004

Sequence 1910, 25 Sequence 106, App Sequence 2041, App Sequence 90, Appl Sequence 400, Appl Sequence 299, Appl Sequence 271, Appl Sequence 271, Appl Sequence 1757, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 107, Appl Sequence 1107, Appl Sequen

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Sequence 18, Appl Sequence 26, Appl Sequence 192, Appl Sequence 18, Appl Sequence 208, Appl Sequence 2046, Appl Sequence 2046, Appl

Sequence 104, App

Sequence 383,

Sequence Sequence

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ALIGNMENTS

Sequence 1397, Apsorted 59, Appl

Sequence 59, Sequence 18,

179264

Sequence Sequence

US-10-204-708-66 US-10-240-595-1910 US-10-311-455-1910 US-10-311-455-1609 US-10-311-455-1609 US-10-311-455-1609 US-10-311-455-299 US-10-311-455-299 US-10-311-455-299 US-10-311-455-299 US-10-311-455-110 US-10-239-676-95 US-10-239-676-95 US-10-239-676-95 US-10-239-676-95 US-10-239-676-189 US-10-239-676-189 US-10-240-453-109 US-10-240-453-109 US-10-240-453-109 US-10-240-453-109 US-10-240-453-109 US-10-240-453-109 US-10-240-453-109 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139 US-10-211-455-139

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10:27:15 ; Search time 535.761 Seconds (without alignments) 10091.039 Million cell updates/sec
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
7 /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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No.
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RESULT 1 US-10-211-179-11 GENERAL INFORMATION: APPLICANT: Nicholas M. Dean APPLICANT: Kenneth M. Dobie TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOTYRO FILE REPRENCE: PTS-0011 CURRENT APPLICATION NUMBER: US/10/211,179 CURRENT FILING DATE: 2002-08-01 NUMBER OF SEQ ID NOS: 119 OTHER INFORMATION: n = a, t, c, or g US-10-211-179-11	Query Match 5.6%; Score 55.6; DB 16; Best Local Similarity 42.6%; Pred. No. 0.67; Matches 346; Conservative 1; Mismatches 460;	OY 117 AGAGAAGAITAAAIGTGAIGTYCATICAAGAITCAAGAICAIT	Qy 177 CAAGGAATAAATAACGATAAATGAGATTAAAGTAAATAAGGAGA	VII Db 22184 TAATATATAATATATATATATATATATATATATATATA	Ap 237 IGAATGAGGTGGATGATTCTTTTTTGACAATGATGATGATGATGATGATGATGATGATGATGATGATG	App Db 22244 ATAATAAAAAAAAATATAAAATATATAAAAATATATAAAA	AP 297 ITGGGACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAG	App Db 22304 ATAAATATATATATATATATATATATAAATATATATAT	APP APP APP APP APP APP APP APP APP APP
OMB. seq: * COMB.	dicted by chance to have a re of the result being printed, 1 score distribution.		Description	GENERAL INFORMATI	Sequence 2148, Ap Sequence 2148, Ap	588,	Sequence 5738, 7	Sequence 2, Appliance 418, App	sequence 205, App Sequence 422, App Sequence 2, Appl
/cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US09E_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US0A_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:* /cgn2_6/ptodata/2/pubpna/US10_NUB_PUB.seq:*	the number of results predicted by chance to than on equal to the score of the result being dby analysis of the total score distribution	SUMMARIES	DB ID	16 US-10-211-179-11 17 HS-10-433-793-28	15 US-10-311-455-2148 15 US-10-340-485-64		US-10-741-	US-10-221-7	15 US-10-240-453-206 16 US-10-221-714A-422 15 US-10-312-841-2
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GATAATCGAATCTCTTT TATATATATATAT TTCAAAGAATATTTTA

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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIPENBROCK, Christian
APPLICANT: PIPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determi
TITLE OF INVENTION: cytosine methylation
TITLE OF INVENTION: cytosine methylation
FILE REPERBNCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2001-07-02
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 2424
SEQ ID NOS: 2424
                                                                                                                                                                   11860 Tradatradadadacaaratadadadacarretracradeceradadecarritrata 11801
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                                                                                                    tracaatataaaatattacitta---cractataatcaaatrcacacciacaacgraact
                                       11976 TAAAATTCATATTAAATTTTAATTTTACCGATAT-TTÄTTTTTÄCTTAÄCACTAÄATCTC
                                                                                                                                                                                                    CTAAGGAGTAAAGCAACCATGAATAGAAAAGGCTTAGTAACTATATATCAAAGGAATGGT
                                                                       TCACTITICTACGATACTGCTTCATGTCAAATCTTAATGAAAGCAGATTTTGACCCATACA
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5.4%; Score 54.4; DB 15;
Best Local Similarity 46.1%; Pred. No. 1.1;
Matches 178; Conservative 1; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2148, Application US/10311455 Publication No. US20030143606A1 GENERAL INFORMATION:
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US-10-311-455-2148/c
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US-10-433-793-28/C
US-10-433-793-28/C
Sequence 28, Application US/10433793
Sequence 28, Application No. US20040142334A1
Sequence 28, Application No. US20040142334A1
Sequence 28, Application No. US20040142334A1
Sequence 28, Application No. US20040142334A1
Sequence 28, Application NowBER: US/10/433,793
CURRENT PILING DATE: 2003-06-06
NUMBER OF SEQ ID NOS: 212
SEQ ID NO 28
LENGTH: 37515
                            TCAGAGAATATTACATCCCCCTCTCCCTATCTCTTTTTCTATTTATATGGGACATTCC
                                                             AACAIGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGAAAGAICTGAATTTATTAT
                                                                                                                                                                                                                                                                                                                                                                                   AAGAATAGTGTTTTTTTTTTTTTTTTTTTTAAGGAGTAAAGCAACCATGAATAGAA
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                                                                                                                                                                                                                                                                                         AATCTTAATGAAAGCAGATTTTGACCCATACAATAATATGACAAAAATTGCTTCCAAAGAA
                                                                                             TCAATCAATCCTAAAAGTACATACACCAAGAATATTCAATAAAATATTTTTTGAATATT
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                                   3747 AAAATATACCTATTTTTATAATAATATTTTTTTTTAAAATATTTAACAATTCCAC 3688
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                                                                           693 TATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATATCGTTAGACTGTT 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               689 ATAATATGACAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATATCGTTAGAC 748
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GENERAL INV CLEX, Alexander
APPLICANT: DIEDENBROCK, Christian
APPLICANT: DIEDENBROCK, Christian
APPLICANT: BEELIN, Kurt
TILE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Metastasis
FILE REFERENCE: 5013.1007
CURRENT APPLICATION NUMBER: US/10/240,485
CURRENT APPLICATION NUMBER: DE 10019058.8
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
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Pred. No. 0.86;
0; Mismatches 99;
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                                                                                                                                                         813 GGAGTAAAGCAACCATGAATAGAAAA 838
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Publication No. US20030148327A1
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Best Local Similarity
Matches 112; Conserv
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US-10-311-455-588
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TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determorating OF INVENTION: Octosine methylation rights of INVENTION: Octosine methylation rights of INVENTION: Octosine methylation rights of INVENTION: Octosine methylation rights of Invention with the Invention with the Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of Invention of In
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Pred. No. 1.4;
1; Mismatches 296; Indels
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; Publication No. US20040166519A1
; RENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
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Best Local Similarity 46.6%;
Matches 264; Conservative
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US-10-741-601-5686/c
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Publication No. US20030143606A1
PRERAL INFORMATION:
APPLICANT: OLEK, Alexander
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APPLICANT: Epigenomics AG
APPLICANT: Epigenomics AG
FILE REPERENCE: Epigenomics AG
FILE REPERENCE: E01/1208/WO
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
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2 ATATAGACTTTTGATTAAATTAATTATTGTATGACAAAGGATTAAACCTAGTTAATG
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                                                                              62 ATAATAACTTCAGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGCGTTGAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                     302 ACCCTTCTCGGATCTAATGAAAAAGTATGGAATAGTAGTAGATAATCGAATCT 352
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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Pred. No. 19;
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ORGANISM: Artificial Sequence
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Best Local Similarity
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LOCATION: (379615)
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US-10-312-841-2
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OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
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Sequence 5738, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC FOLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPERSENCE: CLOO1500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FastSEQ for Windows Version 4.0
  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 27890
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                                                                                                                                                                                                                                                                                                                                                    DB 17; Length 27890;
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                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                Ouery Match
Sect Local Similarity 46.4%; Pred. No. 2.6;
Matches 163; Conservative 1; Mismatches
                                                                                                                                                                                                                                                  NAME/KEY: misc_feature;

CCATION: (1)...(27890)

OTHER INFORMATION: n = A,T,C or G,

US-10-741-601-5686
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-741-601-5738
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LENGTH: 126872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-741-601-5738
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Matches 163;
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APPLICANT: PIEDENBROCK, Christian
APPLICANT: PIEDENBROCK, Christian
APPLICANT: PIEDENBROCK, Christian
APPLICANT: PIEDENBROCK, Christian
APPLICANT: BRILIN, RUL
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Assessing the Methylation Status of Genes Associated
TITLE OF INVENTION: With DNA READSCRIPTION
FILE REPRENCE: 5013.1009
CURRENT FILING DATE: 2001-040
FRIOR APPLICATION NUMBER: DCT/ZPO1/03973
PRIOR PILING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
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PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-06-01
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PRIOR PILING DATE: 2000-06-01
PRIOR PILING DATE: 2000-08-01
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                                                   5899 САТТТААТААТТААААТТСТТТААТААТСААТААТТАААБАТСТАТАААААТТААТААТ 5840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192 GATAAATGGCATTAAAGTAAATAAGGAGAATGATTCACCCAATATTGAATGAGGTGGATG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6199 ТТААСАЯТЯТСТТТААААЯТСААТААТААТАААААААТССААТАААААА
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 AGATCTATAATCAATTAACAGCAATCACGGTCATAGCAGC-GTTGAGAAGATTAAATG
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5.0%; Score 50; DB 15; Length 11
Best Local Similarity 47.9%; Pred. No. 3.6;
Matches 202; Conservative 1; Mismatches 216; Indels
      TAGAAAAGGCTTAGTAACTATATATCAAAGGAATGGTGT
                                                                                                                                                                      502 Arriririarararahakkararrirararrarar
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                                                                                                                892 AAATTTGTGAATATAGAAGATTAGATCAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (9105)
                                                                                                                                                                                                                                                                                             US-10-240-453-206/c
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   832
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1067947 TTTTTTTTTTAATTTTTAAAATTATTTTTTTGTTATAGTTTGGGTTATGTATATTTATGG 1068006
                                                                                                             AAAGCAACCATGAATAGAAAAGGCTTAGTAACTATATATCAAAGGAATGGTGTTTTTTCT 877
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                                                      CAAAATTGCTTCCAAAGAAAACATGGCTCTTATAGTGAAATATCGTTAGACTGTTATAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 418, Application US/10221714A

Sequence 418, Application US/10221714A

Publication No. US20040048254A1

SEQUENCE INFORMATION:

APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005

CURRENT APPLICATION NUMBER: US/10/221,714A

CURRENT APPLICATION NUMBER: DE 10019055

PRIOR APPLICATION NUMBER: DE 10019058 B

PRIOR APPLICATION NUMBER: DE 10019058 B

PRIOR PILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: DE 10013529,7

PRIOR FILING DATE: 2000-06-30

PRIOR SEDING DATE: 2000-06-30

PRIOR SEDING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 540

SEQ ID NO SEQ ID DOS: 540
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Best Local Similarity 51.3%; Pred. No. 4.8;
Matches 139; Conservative 0; Mismatches 131; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
, OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-221-714A-422
                                                                                                                                                                                                    Sequence 422, Application US/10221714A

Publication No. US20040048254A1

GENERAL INFORMATION:
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Diagnosis of Diseases Associated
CURRENT FILING DATE: 2003-01-21
PRIOR PILING DATE: 2003-01-21
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-16
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR PILING DATE: 2000-03-07
PRIOR APPLICATION NUMBER: DE 100131259.7
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 540
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                                                                                                                5779 AA 5778
                                                                         430 CA 431
370
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US-10-312-841-2/c; Sequence 2, Application US/10312841; Publication No. US20030186277A1

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des WHC
TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des WHC
FILE REFERENCE: B01/1206/WO
FURENT BPLICATION NUMBER: US/10/312,841
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 3673778
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Sequence 66, Application US/10204708

Publication No. US20030141852A1

Sequence 66, Application US/10204708

Publication No. US20030141852A1

Sequence 66, Application US/10204708

Publicant OLEK, Alexander

APPLICANT: PIEBENBROCK, Christian

APPLICANT: DIREBENBROCK, Christian

APPLICANT: DIREBENBROCK, Christian

APPLICANT: DIREBENBROCK, Christian

APPLICANT: DIREBENBROCK, Christian

APPLICANT: DIAGOUSE OF DISCOURT OF TILLE OF INVENTION: DAY ASSESSING DNA Methylation

FILE REFERENCE: 5013.1012

CURRENT APPLICATION NUMBER: US/10/204,708

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019058.8

PRIOR APPLICATION NUMBER: DE 10019173.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

PRIOR FILING DATE: 2000-06-07

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PRIOR FILING DATE: 2000-06-07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 TTTTGACAATGATGATGATGGCCAAATACTAGAATGTTGGGACCCTTCTCGGATCTAAT 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      320 GAAAAAAGTATGGAATAGTAGATAATCGAATCTCTTTAGAAAGGTAGTGATTGTCTTTTA 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3673778;
                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

4.9%; Score 49.4; DB 15; Length
Best Local Similarity 47.3%; Pred. No. 50;
Matches 181; Conservative 0; Mismatches 201; Indels
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                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                         ) NAME/KEY: unsure
) LOCATION: (379615)
US-10-312-841-2
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1913 GTTTTTAAAAACGTTAGGAAAGAGTATATATTAATGAAGTATTTTTTATGGGTAATATTA 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1913 GTTTTTAAAAACGTTAGGAAAGAGTATATAATGAAGTATTTTTTATGAGGTAATATTA 1972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-240-589C-106
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                                                                                                                                                                                                                                                 APPLICANT: OLEK, Alexander
APPLICANT: DIEBRIBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: DAG ASSOCIATED With
TITLE OF INVENTION: DNA repair
FILE REFERENCE: 5013.1008
CURRENT APPLICATION NUMBER: US/10/240,589C
CURRENT FILING DATE: 2003.09.02.
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4.9%; Score 49.2; DB 16;
Best Local Similarity 52.4%; Pred. No. 3.8;
Matches 108; Conservative 0; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT FILING DATE: CO13-09-02

PRIOR APPLICATION NUMBER: PCT/EPO1/03972

PRIOR FILING DATE: 2001-04-06

PRIOR ALFLICATION NUMBER: DE 10019058.8

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-06

PRIOR FILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR PILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 148
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                                                                                     1973 AAGTIGITITATITIGIAATIGGAAT 1998
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                                                864 ATGGTGTTTTTTTAAATATGGAT
                                                                                                                                                                                        Sequence 106, Application US/10240589C Publication No. US20040076956A1 GENERAL INFORMATION:
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                                                                                                                                                RESULT 15
US-10-240-589C-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               804 CATATCTAAGGAGTAAAGCAACCATGAATAGAAAAGGCTTAGTAACTATATCAAAGGA 863
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                                                                                                                                                                                                           Query Match 4.9%; Score 49.2; DB 15; Length 5360; Best Local Similarity 52.4%; Pred. No. 3.8; Matches 108; Conservative 0; Mismatches 98; Indels 0;
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4.9%; Score 49.2; DB 15; Length 5360;
Best Local Similarity 52.4%; Pred. No. 3.8;
Matches 108; Conservative 0; Mismatches 98; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1973 AAGTIGITITATITIGIAATIGGAAT 1998
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 66
LENGTH: 5360
TYPE: DNA
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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